

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2005, 22:42:53 ; Search time 21.0928 Seconds
(without alignments)
1806.392 Million cell updates/sec

Title: US-10-732-923-406

Perfect score: 2118

Sequence: 1 MTVTIKELTNHYIDHELSEA.....KIVYDLDYHLYFMKLQKKI 396

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2118	100.0	396	1	adenosylmethionine
2	479	22.6	333	1	adenosylmethionine
3	479	22.6	334	1	adenosylmethionine
4	478	22.6	334	2	adenosylmethionine
5	476	22.5	335	2	adenosylmethionine
6	470	22.2	334	1	adenosylmethionine
7	434	20.5	368	2	adenosylmethionine
8	404	19.1	362	2	adenosylmethionine
9	401.5	19.0	353	2	adenosylmethionine
10	398.5	18.8	357	2	adenosylmethionine
11	387	18.3	369	2	adenosylmethionine
12	378	17.8	393	2	adenosylmethionine
13	376.5	17.8	381	2	adenosylmethionine
14	372.5	17.6	400	2	adenosylmethionine
15	359	16.9	361	2	adenosylmethionine
16	348.5	16.5	377	2	adenosylmethionine
17	343	16.2	360	2	adenosylmethionine
18	341.5	16.1	361	2	adenosylmethionine
19	331	15.6	363	2	adenosylmethionine
20	313	14.8	398	2	adenosylmethionine
21	110.5	5.2	900	2	adenosylmethionine
22	108	5.1	1576	1	adenosylmethionine
23	107	5.1	1034	2	adenosylmethionine
24	106.5	5.0	1028	2	adenosylmethionine
25	104	4.9	958	2	adenosylmethionine
26	103	4.9	1126	2	adenosylmethionine
27	102.5	4.8	1004	2	adenosylmethionine
28	101	4.8	518	2	adenosylmethionine
29	100.5	4.7	773	2	adenosylmethionine

30	100	4.7	1294	2	T18473
31	99.5	4.7	810	2	B71639
32	99.5	4.7	1204	2	T18812
33	99	4.7	498	2	G97279
34	99	4.7	1456	2	S14005
35	98.5	4.7	1028	2	G64595
36	98	4.6	358	1	W2WL58
37	97.5	4.6	342	1	S29133
38	97	4.6	317	2	A81320
39	97	4.6	580	2	T01865
40	96.5	4.6	408	2	B90517
41	96.5	4.6	1189	2	T30319
42	96	4.5	628	2	S41138
43	96	4.5	971	2	A70179
44	95.5	4.5	502	2	E89767
45	95.5	4.5	525	2	T44074

ALIGNMENTS

RESULT 1

DCBYDM

adenosylmethionine decarboxylase (EC 4.1.1.50) precursor - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein O1275; protein YOL052c

C;Species: Saccharomyces cerevisiae
C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text change 09-Jul-2004
C;Accession: S12772; A30469; S59299; S61729; S66737; S66744

R;Kashiwagi, K.; Taneja, S.K.; Liu, T.Y.; Tabor, C.W.; Tabor, H.

J. Biol. Chem. 265, 22321-22328, 1990

A;Title: Spermidine biosynthesis in Saccharomyces cerevisiae. Biosynthesis and processing

A;Reference number: S12772; MUID:91093074; PMID:2266128

A;Accession: S12772

A;Molecule type: DNA

A;Residues: 1-396 <KAS1>

A;Cross-references: UNIPROT:P21182; EMBL:M38434; NID:gl71054; PIDN:AAA34421.1; PID:gl710

A;Accession: A30469

A;Molecule type: protein

A;Residues: 2-19; 'A', 89-101, 'X', 103-104 <KAS2>

R;Mannhaupt, G.; Vetter, I.; Schwarzlöse, C.; Mitzel, S.; Feldmann, H.

submitted to the EMBL Data Library, August 1995
A;Description: Analysis of a 26kb region on the left arm of yeast chromosome XV.

A;Reference number: S59285

A;Accession: S59299

A;Molecule type: DNA

A;Residues: 1-396 <FEL>

A;Cross-references: EMBL:X91067; NID:g984177; PIDN:CAA62536.1; PID:g984192

R;Mannhaupt, G.; Vetter, I.; Schwarzlöse, C.; Mitzel, S.; Feldmann, H.

Yeast 12, 67-76, 1996

A;Title: Analysis of a 26 kb region on the left arm of yeast chromosome XV.

A;Reference number: S61715; MUID:96381248; PMID:8789261

A;Accession: S61729

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-396 <MAN>

A;Cross-references: EMBL:X91067; NID:g984177; PIDN:CAA62536.1; PID:g984192

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995

R;Ansorge, W.; Benes, V.; Rechmann, S.; Schwager, C.; Teodoru, C.; Voss, H.; Wiemann, S.

submitted to the Protein Sequence Database, July 1996

A;Reference number: S66723

A;Accession: S66737

A;Molecule type: DNA

A;Residues: 1-396 <ANS>

A;Cross-references: EMBL:Z74794; NID:gl1419858; PIDN:CAA99058.1; PID:gl1419859; GSPDB:GN000

R;Feldmann, H.; Mannhaupt, G.; Vetter, I.

submitted to the Protein Sequence Database, July 1996

A;Reference number: S66743

A;Accession: S66744

A;Molecule type: DNA

A;Residues: 1-396 <FEW>

A;Cross-references: EMBL:Z74794; NID:gl1419858; PIDN:CAA99058.1; PID:gl1419859; GSPDB:GN000

A;Experimental source: strain S288C

C;Comment: The pyruvyl group derived from 88-Ser is required for catalytic activity and C;Genetics:

A;Gene: SGD:SPE2; MIPS:YOL052C
A;Cross-references: SGD:S0005412; MIPS:YOL052C
A;Map position: 15L
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase; polyamine biosynthesis
F;2-87/Domain: beta chain #status experimental <CHB>
F;2-87/Domain: beta chain #status experimental <CHB>
F;2-87/Domain: alpha chain #status experimental <CHA>
F;88-396/Domain: pyruvic acid (Ser) (in mature form) #status experimental

Query Match 100.0%; Score 2118; DB 1; Length 396;
Best Local Similarity 100.0%; Pred. No. 7e-154; Indels 0; Gaps 0;
Matches 396; Conservative 0; Mismatches 0;

QY 1 MTVTIKELTNHNTIDHLSATLSDTAPEGEPEKLEIWFPPHKKSIITTEKTLRNIGMDRW 60
DB 1 MTVTIKELTNHNTIDHLSATLSDTAPEGEPEKLEIWFPPHKKSIITTEKTLRNIGMDRW 60
QY 61 IEILKLVKCVLSMKTKELDALLSSSLFVFDHKLTKMTCTGTTTTLFCLEKLFQIVEQ 120
DB 61 IEILKLVKCVLSMKTKELDALLSSSLFVFDHKLTKMTCTGTTTTLFCLEKLFQIVEQ 120
QY 121 ELSWAFRTTGGKYKPKFVSRRCFLPCKQAAIHQNWADVDYLNKFPDNGKSYSGR 180
DB 121 ELSWAFRTTGGKYKPKFVSRRCFLPCKQAAIHQNWADVDYLNKFPDNGKSYSGR 180
QY 181 NDKSNHNLVVTETDRSTPKGEYIEDDDTFEVLMTPELDEPCASFVCGPEASTTALVE 240
DB 181 NDKSNHNLVVTETDRSTPKGEYIEDDDTFEVLMTPELDEPCASFVCGPEASTTALVE 240
QY 241 PNEDKGHNLYQMTKNTRLDEIYVNSAQSDLSFHHDAFAFTPCGYSSNMILAEKYITL 300
DB 241 PNEDKGHNLYQMTKNTRLDEIYVNSAQSDLSFHHDAFAFTPCGYSSNMILAEKYITL 300
QY 301 HVTPEKGWSYASFSNIPVDFISQGDNDLVLLHILNVFPREFSMFTTKYQNSQFQ 360
DB 301 HVTPEKGWSYASFSNIPVDFISQGDNDLVLLHILNVFPREFSMFTTKYQNSQFQ 360
QY 361 KLLSINESLPDYIKLDKIVYDLDYHLFYMKLQKKI 396
DB 361 KLLSINESLPDYIKLDKIVYDLDYHLFYMKLQKKI 396

RESULT 2
DCRTDM
adenosylmethionine decarboxylase (EC 4.1.1.50) precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: JQ0439; B31786; F51487; A47002
R;Pulkka, A.; Keraenen, M.R.; Salmela, A.; Salmikangas, P.; Ihalaenen, R.; Pajunen, A.
Gene 86, 193-199, 1990
A;Title: Nucleotide sequence of rat S-adenosylmethionine decarboxylase cDNA: comparison
A;Reference number: JQ0439; MUID:90215298; PMID:2323572
A;Accession: JQ0439
A;Molecule type: mRNA
A;Residues: 1-333 <PUL>
A;Cross-references: UNIPROT:P17708; GB:M34464; NID:g202754; PIDN:AAA40683.1; PID:g202755
R;Pajunen, A.; Crozat, A.; Jaenne, O.A.; Ihalaenen, R.; Laitinen, P.H.; Stanley, B.; Mad
J. Biol. Chem. 263, 17040-17049, 1988
A;Title: Structure and regulation of mammalian S-adenosylmethionine decarboxylase.
A;Reference number: A92685; MUID:89034205; PMID:2460457
A;Accession: B31786
A;Molecule type: mRNA
A;Residues: 1-4, 'P', 6-145, 'A', 147-333 <PAJ>
A;Cross-references: GB:M34464
R;Pulkka, A.; Ihalaenen, R.; Aatsinki, J.; Pajunen, A.
FEBS Lett. 291, 289-295, 1991
A;Title: Structure and organization of the gene encoding rat S-adenosylmethionine decarboxylase
A;Reference number: S18487; MUID:92038054; PMID:1936275
A;Accession: S18487
A;Status: translation not shown

A;Molecule type: DNA
A;Residues: 1-145, 'A', 147-333 <PU2>
A;Cross-references: GB:M64274; NID:g206843; PIDN:AAA42105.1; PID:g206844
R;Pulkka, A.; Ihalaenen, R.; Suorsa, A.; Riviere, M.; Szpirer, J.; Pajunen, A.
Genomics 16, 342-349, 1993
A;Title: Structures and chromosomal localizations of two rat genes encoding S-adenosylme
A;Reference number: A47002; MUID:93300506; PMID:8314573
A;Accession: A47002
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-145, 'A', 147-333 <RES>
A;Cross-references: EMBL:Z15109; NID:g55705; PIDN:CAA78814.1; PID:g818018
C;Comment: The proenzyme is cleaved after translation into an alpha chain and a beta cha
quired for enzyme activity. The active enzyme catalyzes the decarboxylation of S-adenos
C;Comment: This is a key enzyme in the biosynthesis of polyamine.
C;Genetics:

A;Gene: AMD1B
A;Introns: 37/2; 66/2; 108/3; 143/1; 157/2; 236/3; 288/3
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase; polyamine biosynthesis
F;1-67/Domain: alpha chain #status predicted <CHA>
F;1-67,68-333/Product: adenosylmethionine decarboxylase #status predicted <MAT>
F;68-333/Domain: beta chain #status predicted <CHB>
F;68/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 22.6%; Score 479; DB 1; Length 333;
Best Local Similarity 30.3%; Pred. No. 5e-29; Indels 56; Gaps 10;
Matches 117; Conservative 68; Mismatches 138;

QY 22 LDSTAFEGPEKLEIWFPPHKKSIITTEKTLRNIGMDRWIEILKLVKCVLSMKTKEK 80
DB 1 MEAAHFEGETKLELVFWSRQSDASQSGDLATIPRSEWDVLLKDVQCSIIISVTIKDQ 60
QY 81 DAPLSESSLFVFDHKLTKMTCTGTTTTLFCLEKLFQIVEQELSWAFRTTGGKYKPF--- 137
DB 61 EAYLVSESSMFVSRFRILKTCGTGTTLLKALVPLLLARD-----YSGFDSI 107
QY 138 -KVYFSRRCLFPCKQAAIHQNWADVDYLNKFPDNGKSYSGRNDKSNHNLVVTETDR 196
DB 108 QSPFYSRKFMKPSHQGYPHRNFQEEIEFLNLPNGAGYCMGRMN-SDCWYLYTLDLPE 166
QY 197 STPKGEYIEDDDTFEVLMTPELDEPCASFVCGPEASTTALVEPNEDKGHNLYQMTKN 256
DB 167 S-----RVINQPDQTLLEILMSELDPAVMDQFYM-----KQGVTAQDVTR 206
QY 257 TRLDEIYVNSAQSDLSFHHDAFAFTPCGYSSNMILAEKYITLHVTPEKGWSYASFSN 316
DB 207 SGIRDLIPGSVIDATL-----FNPCGYSMNGMKS DGTWTYTHITPEPEFSYVSEFN 258
QY 317 IPVFDISQGDNDLVLLHILNVFPREFSMFTTKYQNSQFQKLLSINESLPDYIKLD 376
DB 259 -----LSQTSYD--DLIRKVVVEFKGKFTVTLFVN--QSSKRTVLSSPQKIDGFKRLD 309
QY 377 KIVYDLDYHLFYMKLQKK 395
DB 310 CQSAMFNDYNFVFTSPAKK 328

RESULT 3
DCHYDM
adenosylmethionine decarboxylase (EC 4.1.1.50) precursor - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: S22358; S19871
R;Tekwani, B.L.; Stanley, B.A.; Pegg, A.E.
Biochim. Biophys. Acta 1130, 221-223, 1992
A;Title: Nucleotide sequence of hamster S-adenosylmethionine decarboxylase cDNA.
A;Reference number: S22358; MUID:92223099; PMID:1562599
A;Accession: S22358
A;Molecule type: mRNA
A;Residues: 1-334 <TEK>
A;Cross-references: UNIPROT:P28918; EMBL:X63861; NID:g55521; PIDN:CAA45343.1; PID:g55522
A;Experimental source: liver of Syrian golden hamster

[illegible]

C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;71/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 18.8%; Score 398.5; DB 2; Length 357;
Best Local Similarity 33.0%; Pred. No. 7.5e-23;
Matches 121; Conservative 65; Mismatches 122; Indels 59; Gaps 16;

QY 24 STDAFEGPEKLLIWIWPPHKKSIITTE---KTLRNIGMDRWIEILKLVKCEVLSMKTKEL 80
DB 6 SAIGFEGYKRLIISFF--ESSFFADPDGKGLALNKSQIDEILEPAECTIVDSLNSQYL 63
QY 81 DAFLLSESLFVFDHKLTKMTCTGTTTLFLEKLFQIVEQELSWAFRTTQGGKYKPKVF 140
DB 64 DSVVLSSESLFVVPYKIIKTGTTTKLLSIPAILKAE--SLSLSVR-----NVK 112
QY 141 YSRRCFLFPCKQAAIHQNWADVDYLNKFFD----NGKSYSVGRNDKSNHNLVYTTETDR 196
DB 113 YTRGSFIFFCAQSPHRSFSEVEILLDNYFGKLGLESNAFIMGNDPQPKWHVY----- 166
QY 197 STPKGYEIEDDDTEFEVLMTLDPCEASKFVCGPEASITATLVEPNEDKGNHLYQWTKN 256
DB 167 SASVGSQSSDPTTYLTEMCTGTDREKASVYF--KSESSAAL-----MTTR 211
QY 257 TRIDEIYVNSAQSDLSFHHDFAFTPCGYSSNMILAEKYTYTLHTVPEKGMWYAGFESN 316
DB 212 SGIRKI-----LPSEIC----DEFFPCGYSMNSI--EAAISTIHVTPEDGFYASFEA- 261
QY 317 IPVFDISQGGQKQDNLVLL--HILNVQFPRFSMTFTTKNYQNSQFQKLLSINESLPDIYKL 375
DB 262 -AGYDL--KAQNLGMWIERVACLPQSPSESVAVHC-DVTCKSLQICSL--ELKEYSLD 314
QY 376 DKIVYDL 382
DB 315 EKINEEL 321

RESULT 11
T10750
probable adenosylmethionine decarboxylase (EC 4.1.1.50) - leaf mustard
C;Species: Brassica juncea (leaf mustard)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10750
R;Lee, T.; Liu, J.J.; Pua, B.C.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z17116
A;Accession: T10750
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-369 <LEE>
A;Cross-references: UNIPROT:Q49972; EMBL:U80916; NID:G2662405; PID:G2662406
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;69/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 18.3%; Score 387; DB 2; Length 369;
Best Local Similarity 31.4%; Pred. No. 5.9e-22;
Matches 116; Conservative 60; Mismatches 126; Indels 68; Gaps 13;

QY 24 STDAFEGPEKLLIWIWPPHKKSIITTE---KTLRNIGMDRWIEILKLVKCEVLSMKTKELDA 82
DB 4 SAIGFEGYKRLIISFF--ESSFFADPDGKGLALNKSQIDEILEPAECTIVDSLNSDELDS 63
QY 83 FLVLSSESLFVFDHKLTKMTCTGTTTLFLEKLFQIVEQELSWAFRTTQGGKYKPKVFYS 142
DB 64 YVLSSESLFIPYKIIKTGTTTKLLSIPAILKAE--SLSLSVR-----VRYT 112
QY 143 RRCFLPCKQAAIHQNWADVDYLNKFFD----NGKSYSVGRNDKSNHNLVYTTETDRST 198
DB 113 RGSFLCPGCGPFFHRSFSEVSLDGHFAKMGVSSVAYLMDGDDDETKWHVYASAPARN 172
QY 199 PKGKEYIEDDDTEFEVLMTLDPCEASKFVCGPEASITATLVEPNEDKGNHLYQWTKNTR 258

DB 173 GNGNN--NNVYLTLEMCTGLDKEKASVFKNESSAGS-----MTDNGS 215
QY 259 LDRIYVNSAQSDLSFHHDFAFTPCGYSSNMILAEKYTYTLHTVPEKGMWYASFEES--- 315
DB 216 IRKILPQS-QICD-----FEPEPCGYSNWSVEGDA-ISTIHVTPEDEGYSASFVAVGY 266
QY 316 NIDVFDISQGGQKQDNLVLLHILNVQFPRFSMTFTTKNYQNSQFQKLLSINESLPDIYKL 375
DB 267 DFTMDLSH-----LVSKVLTCTFEKQFSVAHVSSVAQ-KSYDGLSLV----- 308
QY 376 DKIVYDLDDY 385
DB 309 -----DLEDY 313

RESULT 12
S69191
adenosylmethionine decarboxylase (EC 4.1.1.50) precursor - wild barley
C;Species: Hordeum chilense (wild barley)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S69191
R;Dresselhaus, T.; Barcelo, P.; Hagel, C.; Loefer, H.; Humbeck, K.
Plant Mol. Biol. 30, 1021-1033, 1996
A;Title: Isolation and characterization of a Tritordeum cDNA encoding S-adenosylmethionine
A;Reference number: S69191; MUID:96270379; PMID:8639739
A;Accession: S69191
A;Molecule type: mRNA
A;Residues: 1-393 <DRE>
A;Cross-references: UNIPROT:Q42829; EMBL:X83881; NID:G1403043; PID:CAA58762.1; PID:G1403043
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;71/Product: adenosylmethionine decarboxylase beta chain #status predicted <MAT1>
F;72-393/Product: adenosylmethionine decarboxylase alpha chain #status predicted <MAT2>
F;247-262/Region: PEST sequence
F;71/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 17.8%; Score 378; DB 2; Length 393;
Best Local Similarity 30.4%; Pred. No. 3.1e-21;
Matches 116; Conservative 55; Mismatches 122; Indels 88; Gaps 16;

QY 24 STDAFEGPEKLLIWIWFF-----PHKKSITTEKTLRNIGMDRWIEILKLVKCEVLSMKK 76
DB 6 SAIGFEGYKRLIISFF--ESSFFADPDGKGLALNKSQIDEILEPAECTIVSEL 59
QY 77 TKELDAFLSESLFVFDHKLTKMTCTGTTTLFLEKLFQIVEQELSWAFRTTQGGKYK 136
DB 60 NKDFDVSLSSESLFIYSQKIVTKTCTGTTLLTIPRIELAE--ELCMPLAA----- 110
QY 137 FKVFYSRRRCFLFPCKQAAIHQNWADVDYLNKFF---DNKSYSVGRNDK-SNHNLVY 191
DB 111 --VKYSGWFIFFCAQAPAPHRSPSEVDVNLRYFGLHNSGNAYVICDPAPKQKWHIY 168
QY 192 TETDRSTPKGKEYIEDDDTEFEVLMTLDPCEASKFVCGPEASITATLVEPNEDKGNHLY 251
DB 169 -----ATEQEPQPMVLTLEMCTGLDKEKASVFKNESSAGS-----KTHADGH 203
QY 252 -----QMTKNTRLDEIYVNSAQSDLSFHHDFAFTPCGYSSNMILAEKYTYTLHTVPEK 306
DB 204 VSCAKEMTKLSGSDI-IPMEVCD-----PDFPCGYSMNAINGSA-FSTIHVTPED 254
QY 307 GWSYASFE-SNIPVFDISQGGQKQDNLVLLHILNVQFPRFS---MTFTTKNYQNSQFQKLL 363
DB 255 GFSYASVEYQGMDSALAYG-----DIVKRVLCFGPSEFSVAVTIFGGRGHAATWCK-- 307
QY 364 SINESLPDIYKLDDY 384
DB 308 -----KLDAAEYDCNN 318

RESULT 13
T10707
adenosylmethionine decarboxylase (EC 4.1.1.50) 1 - clove pink
N;Alternate names: S-adenosylmethionine decarboxylase 1

C;Species: Dianthus caryophyllus (clove pink)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10707; T10787
R;Lee, M.M.; Lee, S.H.; Park, K.Y.
submitted to the EMBL Data Library, October 1995
A;Description: Nucleotide sequence of cDNAs encoding S-adenosylmethionine decarboxylase
A;Reference number: Z17089
A;Accession: T10707
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-381 <LSE>
A;Cross-references: UNIPROT:Q39676; EMBL:U30526; NID:g1155239; PID:g1155240
A;Experimental source: cv. White Sim; carnation petal
R;Kim, Y.J.; Lee, M.M.; Chang, K.S.; Lee, S.H.; Park, K.Y.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z17144
A;Accession: T10787
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-381 <KIM>
A;Cross-references: EMBL:U94786; NID:g2406584; PID:g2406585
A;Experimental source: strain White sim
C;Genetics: Gscd9
C;Function: Gscd9
A;Description: catalyzes the decarboxylation of S-adenosyl-L-methionine to (S)-deoxy-5-adenosylmethionine
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;93/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 17.8%; Score 376.5; DB 2; Length 381;
Best Local Similarity 31.2%; Pred. No. 3.9e-21;
Matches 112; Conservative 57; Mismatches 123; Indels 67; Gaps 11;

QY 5 IKELTNNY-----IDHLSATLDSTAFEGPEKLLIWIWPPHKKSTTTE-KTLRNI 55
DB 3 VPTLGSNNYTVSPMGDDNNTWAL--SAIGFEGFEKRLIETSPFPGIFVDPGKGLRAL 60
QY 56 GMDRWIELKLVKEVLSMKKTKELDAFLSSESLFVDFHKLTKMTCTGTTTFLCLESKLF 115
DB 61 SKQLDELPGAETCIVDSLANESVDSVLSSESLFYIYKIIKTKGTTKLLHSLPIL 120
QY 116 QIVEQELSWAFRTTQGGKYPKFFVYRRRCFLPCKQAAIHQNWADVDVYLNKFFDN--- 172
DB 121 TLAD-----GLCLDVKSRYRTRGSIFFGAQSYPHRSFSEVAVLDKYFNGLT 169
QY 173 -GKSYSVGRNDKSNHWNLYTETDRSTPKGKEYIEDDDTFEVLMTLDPCEKSKFVCGP 231
DB 170 GSKAFVNGSPAKPKQKHVYSATAPSS-----YDDPVYTLMECMTGLDKGKASVFPKSE 222
QY 232 EASTTALVEPNEDKGNLGMQTKNTLDEIYVNSAQDSDLSPHHDFAFTPCGYSSNMI 291
DB 223 SASAAV-----MTETSGIRKLTPDSATCD-----FDPEPCGYSSNAI 259
QY 292 LAEKYYVTLHVTPEKWSYASFES--NIPVFDISQKQDNLDVLLHILNVFOPREPSM 347
DB 260 EGPA-VSTIHTEDGFSYASFVAVGVYDLKIVDQVQ-----LVERVLCFQPREPSI 310

RESULT 14
T03947
adenosylmethionine decarboxylase (EC 4.1.1.50) - maize
N;Alternate names: S-adenosylmethionine decarboxylase
C;Species: Zea mays (maize)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T03947
R;Michael, A.J.
submitted to the EMBL Data Library, September 1996
A;Reference number: Z15155
A;Accession: T03947
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA

A;Residues: 1-400 <MIC>
A;Cross-references: UNIPROT:O24575; EMBL:Y07767; PIDN:CAA69075.1
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;78/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 17.6%; Score 372.5; DB 2; Length 400;
Best Local Similarity 31.3%; Pred. No. 8.3e-21;
Matches 109; Conservative 53; Mismatches 115; Indels 71; Gaps 14;

QY 20 ATLDSTDA-----PEGPEKLEIWIWFF-----PHKKSITTEKTLNIGMDRWIELK 65
DB 2 AVLSAADASVSAIGFEGYEKRLIETFSAPVFPVDPHGRG-----LRALSRAQIDSVLD 55
QY 66 LVRCEVLSMKKTKELDAFLSSESLFVDFHKLTKMTCTGTTTFLCLESKLFQIVQEQLSWA 125
DB 56 LARCTIVSELNKPDSVLSSESLFYIYKIIKTKGTTKLLTIPRIELEAE-ELSM 114
QY 126 FRTTQGGKYPKFFVYRRRCFLPCKQAAIHQNWADVDVYLNKFF-----DNKSYSVGRN 181
DB 115 LAA-----VKYSRGTFIFFGAQPAPHRFSFSEVAALNRYFGGLKSGGNAYVIGDP 164
QY 182 DK-SNHNWLYVTETDRSTPKGKEYIEDDDTFEVLMTLDPCEKSKFVCGPEASTTALVE 240
DB 165 ARPGQKWHVFEY-----ATEYPPQPMVYNLEMCMTGLDKKACVF-----FK 204
QY 241 PNEDEKGNLGMQTKNTLDEIYVNSAQDSDLSPHHDFAFTPCGYSSNMIKAEKYVTL 300
DB 205 TNADGNTTCAKEMTKLSGISEI-IPMEICD-----FDPEPCGYSSNAIHGSA-FSTI 255
QY 301 HVTPEKWSYASFES-SNIPVFDISQKQDNLDVLLHILNVFOPREPSM 347
DB 256 HVTPEKWSYASFES-SNIPVFDISQKQDNLDVLLHILNVFOPREPSM 347

RESULT 15
T01934
adenosylmethionine decarboxylase (EC 4.1.1.50) - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01934
R;Paramale, S.R.; Ernst, S.G.
submitted to the EMBL Data Library, November 1997
A;Reference number: Z14462
A;Accession: T01934
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-361 <PAR>
A;Cross-references: UNIPROT:O04009; EMBL:AF033100; NID:g2687583; PID:g2687584
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;73/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 16.9%; Score 359; DB 2; Length 361;
Best Local Similarity 33.8%; Pred. No. 7.8e-20;
Matches 113; Conservative 50; Mismatches 121; Indels 50; Gaps 12;

QY 19 SATLDSTDAPEGPEKLEIWIWFF-PHKKSITTEKTLNIGMDRWIELKLVKEVLSMKKT 77
DB 3 SALPVSAIGFEGPEKRLIETFSFPEGLFADPNGLKLSKAQDLDELGLPAECTIVDSLSN 62
QY 78 KELDAFLSSESLFVDFHKLTKMTCTGTTTFLCLESKLFQIVQEQLSWAFRTTQGGKYP 137
DB 63 DDVDSVLSSESLFVYSYKIIKTKGTTKLLAIPPLIKLAE-TLS-----LKQV 111
QY 138 KVPYSRRRCFLPCKQAAIHQNWADVDVYLNKFFD-----NGKSYSVGRNDKSNHWNLYVTE 193
DB 112 DVRYTRGSFTFPGAQSPFPHRHSFSEVAVLDGYFGKLAAGSKAVIMGSPDKAQKWHVY--- 168
QY 194 TDRSTPKGKEYIEDDDTFEVLMTLDPCEKSKFVCGPEASTTALVEPNEDKGNLGM 253
DB 169 ---SASAGPIQSNDPVYTLMECMTGLDREKASVYF-KTEGSSAA-----HM 210

Qy	254	TKNTRLDEIYVNSAQDSDLSEHHDAPAF	PCGYSSNMILAKEYVYTLHVTPEKGWSY	ASP	313
Db	211	TVRSGIRKILPNS-EICD-----	FEFPCGYSMNSIEGAA-LSTIHITPEDGFS	YASP	261
Qy	314	ESNIPVFDISQKQDNLDVLLHILNVFQ	PREFSM		347
Db	262	EA--VGYDMKTMKLGPL--	VERVLACFPDDEFSI		291

Search completed: May 11, 2005, 22:59:04
Job time : 23.0928 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2005, 22:38:57 ; Search time 93.5567 Seconds
(without alignments)
2167.492 Million cell updates/sec

Title: US-10-732-923-406
Perfect score: 2118
Sequence: 1 MTVTIKELTNHNYIDHELSEA.....KIVYDLDYHLYFMKLQKKI 396

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2118	100.0	396	1	DCAM_YEAST
2	1377	65.0	406	2	Q6F885
3	1161.5	54.8	394	2	Q75884
4	955	45.1	367	2	Q6CT94
5	890.5	42.0	434	2	Q6BPN1
6	756	35.7	418	2	Q6C579
7	681	32.2	503	2	Q9Y7F3
8	571	27.0	378	1	DCAM_SCHPO
9	480	22.7	333	1	DCAM_RAT
10	479	22.6	334	1	DCAM_MESAU
11	479	22.6	334	1	DCM1_MOUSE
12	478	22.6	334	1	DCM2_MOUSE
13	478	22.6	334	1	DCM2_MUSSP
14	476	22.5	335	1	DCAM_XENLA
15	473	22.3	334	1	DCAM_BOVIN
16	471.5	22.3	385	2	Q8TLE3
17	471	22.2	347	1	DCAM_DROME
18	470	22.2	334	1	DCAM_HUMAN
19	466	22.0	334	2	Q6N0B2
20	462	21.8	334	2	Q72VU7
21	444	21.0	338	2	Q7Q1V3
22	442.5	20.9	365	1	DCAM_ONCVO
23	434	20.5	368	1	DCAM_CAEEL
24	419.5	19.8	335	2	Q9BLJ5
25	404	19.1	362	1	DCM2_ARATH
26	401.5	19.0	353	1	DCAM_PEA
27	398.5	18.8	357	1	DCAM_CATRO
28	397.5	18.8	353	1	DCAM_VICFA
29	387	18.3	369	1	DCA2_BRAJU
30	387	18.3	369	2	Q6S2S4
31	384	18.1	367	1	DCA3_BRAJU

32	383.5	18.1	358	2	Q852S9
33	383	18.1	361	2	Q6RUQ3
34	381	18.0	361	1	DCAM_DAUCA
35	378	17.8	393	1	DCAM_HORCH
36	376.5	17.8	381	1	DCAM_DIACA
37	376	17.8	392	2	Q9ZFU1
38	375.5	17.7	366	1	DCM1_ARATH
39	375.5	17.7	366	2	Q94Q05
40	375.5	17.7	366	2	Q6QJ69
41	374.5	17.7	362	1	DCAM_IPONI
42	374	17.7	370	2	Q84LA2
43	372.5	17.6	400	1	DCAM_MAIZE
44	368.5	17.4	362	1	DCAM_IPOBA
45	368.5	17.4	368	1	DCA1_BRAJU

AC	P21182	STANDARD;	PRT;	396 AA.
DT	01-MAY-1991	(Rel. 18, Created)		
DT	01-MAY-1991	(Rel. 18, Last sequence update)		
DT	25-OCT-2004	(Rel. 45, Last annotation update)		
DE	S-adenosylmethionine decarboxylase proenzyme	(EC 4.1.1.50) (AdoMetDC)		
DE	(S-adenosylmethionine decarboxylase beta chain)			
DE	adenosylmethionine decarboxylase			
GN	Name=SPE2; OrderedLocusNames=YOL052C; ORFNames=O1275;			
OS	Saccharomyces cerevisiae (Baker's yeast)			
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
OC	Saccharomycetales; Saccharomycetaceae; Saccharomycetes.			
OX	NCBI_TaxID=4932;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RX	MEDLINE=91093074; PubMed=2266128;			
RA	Kashiwagi K., Tanenja S.K., Liu T.-Y., Tabor C.W., Tabor H.;			
RT	"Spermidine biosynthesis in Saccharomyces cerevisiae. Biosynthesis and processing of a proenzyme form of S-adenosylmethionine decarboxylase."			
RT	decarboxylase."			
RL	J. Biol. Chem. 265:22321-22328(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	STRAIN=S288C / FY73;			
RA	MEDLINE=96381248; PubMed=8789261;			
RX	DOI=10.1002/(SICI)1097-0061(199601)12:1<67::AID-YEAS84>3.0.CO;2-F;			
RA	Mannhaupt G., Vetter I., Schwarlose C., Mittel S., Feldmann H.;			
RT	"Analysis of a 26 kb region on the left arm of yeast chromosome XV."			
RL	Yeast 12:67-76(1996).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Ansorge W., Benes V., Rechmann S., Schwager C., Teodoru C., Voss H., Wiemann S.;			
RL	Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: S-adenosylmethionine decarboxylase is essential for normal growth, sporulation, maintenance of ds-RNA virus, biosynthesis of spermine and spermidine.			
CC	-1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S)-deoxy-5-adenosyl(3-aminopropyl)-methylsulfonium salt + CO(2).			
CC	-1- COFACTOR: Pyruvoyl group.			
CC	-1- PATHWAY: Decarboxylation of S-adenosylmethionine provides the aminopropyl moiety required for spermidine and spermine biosynthesis from putrescine.			
CC	-1- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			

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CC -----
DR ENBL; M38434; AAA34421.1; --
DR ENBL; X91067; CAA62536.1; --
DR ENBL; Z74794; CAA99058.1; --
DR PIR; S12772; DCBYDM.
DR HSP; P17707; IJLO.
DR IntAct; P21182; -.
DR GenOnline; 143474; -.
DR SGD; S00003412; SPE2.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IDA.
DR GO; GO:0015940; P:pantothenate biosynthesis; IMP.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 2.
DR TIGRFAMs; TIGR00535; SAM DCase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
KW Decarboxylase; Direct protein sequencing; Lyase; Pyruvate;
KW Spermidine biosynthesis; Zymogen.
FT CHAIN 1 87
FT      S-adenosylmethionine decarboxylase beta
FT      chain.
FT CHAIN 88 396
FT      S-adenosylmethionine decarboxylase alpha
FT      chain.
FT SITE 87 88
FT MOD_RES 88 88
FT ACT_SITE 29 29
FT ACT_SITE 32 32
FT ACT_SITE 102 102
FT ACT_SITE 396 AA; 46232 MW; 8863676CB5636D71 CRC64;
SQ SEQUENCE 396 AA; 46232 MW; 8863676CB5636D71 CRC64;

Query Match 100.0%; Score 2118; DB 1; Length 396;
Best Local Similarity 100.0%; Pred. No. 6.5e-156;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVTIKELTNHNYIDHLSATLSDTDAFEGPEKLEIWFPPHKKSIITTEKTLRNI GMDRW 60
DB 1 MTVTIKELTNHNYIDHLSATLSDTDAFEGPEKLEIWFPPHKKSIITTEKTLRNI GMDRW 60
QY 61 IEILKLVKCEVLSMKTKELDAFLSSESLFVFDHKLTMKTCGTTTTLFCLEKLPQIVEQ 120
DB 61 IEILKLVKCEVLSMKTKELDAFLSSESLFVFDHKLTMKTCGTTTTLFCLEKLPQIVEQ 120
QY 121 ELSWAFRTTGGKYKPKFYSRRCFLFPCQAAIHQNAWDEVDYLNKFPDNGKSVGR 180
DB 121 ELSWAFRTTGGKYKPKFYSRRCFLFPCQAAIHQNAWDEVDYLNKFPDNGKSVGR 180
QY 181 NDKSNHNLVYTTEDRSTPKGKEYIEDDDTFFVLMTELDPCEASKFVCGPEASTTALVE 240
DB 181 NDKSNHNLVYTTEDRSTPKGKEYIEDDDTFFVLMTELDPCEASKFVCGPEASTTALVE 240
QY 241 PNEDKGHNLYGYQMTKNTRLDEIYVNSAQSDLSFHHDAFAFTPCGYSSNMILAEKYTYTL 300
DB 241 PNEDKGHNLYGYQMTKNTRLDEIYVNSAQSDLSFHHDAFAFTPCGYSSNMILAEKYTYTL 300
QY 301 HVTPEKGWSYASFPESNIPVDISQGDNDLVLLHNLVFPQREFSMTFTKYNQNSQFQ 360
DB 301 HVTPEKGWSYASFPESNIPVDISQGDNDLVLLHNLVFPQREFSMTFTKYNQNSQFQ 360
QY 361 KLLSINESLPDYTKLDKIVYDLDYHLYFYMKLQKI 396
DB 361 KLLSINESLPDYTKLDKIVYDLDYHLYFYMKLQKI 396

RESULT 2
Q6FS85 PRELIMINARY; PRT; 406 AA.
AC Q6FS85
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Candida glabrata strain CBS138 chromosome H complete sequence.
GN ORFNames=CAGL0H02607g;

```

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OS Candida glabrata CBS138.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=284593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS138;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boissame A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).
DR EMBL; CR380954; CAG59842.1; -.
DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
DR GO; GO:0008295; P:spermidine biosynthesis; IEA.
DR GO; GO:0006597; P:spermine biosynthesis; IEA.
DR InterPro; IPR00504; RNA rec mot.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 2.
DR TIGRFAMs; TIGR00535; SAM DCase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
DR PROSITE; PS00030; RRM RNP 1; UNKNOWN 1.
DR PROSITE; PS00030; RRM RNP 1; UNKNOWN 1.
SQ SEQUENCE 406 AA; 47686 MW; E970993AFA7209BE CRC64;

Query Match 65.0%; Score 1377; DB 2; Length 406;
Best Local Similarity 62.4%; Pred. No. 2e-98;
Matches 254; Conservative 66; Mismatches 71; Indels 16; Gaps 5;

QY 1 MTVTIKELTNHNYIDHLSATLSDTDAFEGPEKLEIWFPPHKKSIITTEKTLRNI 55
DB 1 MTVTIKELTNHNYIDHLSATLSDTDAFEGPEKLEIWFPPHKKSIITTEKTLRNI 55
QY 56 GMDRWTEILKLVKCEVLSMKTKELDAFLSSESLFVFDHKLTMKTCGTTTTLFCLEKLP 115
DB 61 AVEKVAAILKLVKCEVLSMKTKELDAFLSSESLFVFDHKLTMKTCGTTTTLFCLEKLP 120
QY 116 QIVQEILSWAFRTTGGKYKPKFYSRRCFLFPCQAAIHQNAWDEVDYLNKFPD 172
DB 121 RIVEEELGMDMRACKENGVKPHKVFYSRRRCFLFPCQAAIHQNAWDEVDYLNKFPD 180
QY 173 GKSYSGRNDKSNHNLVYTTEDRSTPKGKEYIEDD-DETFFVLMTELDPCEASKFVCGP 231
DB 181 GSYLVGRSDQSNHNLVYTTETKNWNITDDCGEDDETELEILMTELDTQCAQFSC 240
QY 232 EASTTALVE---PNEDKGHNLYGYQMTKNTRLDEIYVNSAQSDLSFHHDAFAFTPCGYS 287
DB 241 EVKTVESQSDENTSDEGHLSGYKMTNATRLDRVYNN---EKNVSFHHDAFAFTPCGYS 297
QY 288 SNMILAEKYTYTLHVTPEKGWSYASFPESNIPVDISQGDNDLVLLHNLVFPQREFSM 347
DB 298 SNIIMDEEYTYTLHVTPEKGWSYASFPESNIPVDISQGDNDLVLLHNLVFPQREFSM 357
QY 348 TFFTKNYQNSQFQKLLSINESLPDYTKLDKIVYDLDYHLYFYMKLQK 394
DB 358 TFFCKSMNDSFKLMTKTSGEINVTYKORIIYDLDYHLYIRFER 404

RESULT 3
Q75E84 PRELIMINARY; PRT; 394 AA.
ID Q75E84

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AC Q6BPN1;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Debaryomyces hansenii chromosome E of strain CBS767 of Debaryomyces
DE hansenii.
GN ORFNames=DEHA0812826g;
OS Debaryomyces hansenii CBS767.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
OX NCBI_TaxID=284592;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=CBS767;
RC Genoscope;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382137; CAG89078.1; -
DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
DR GO; GO:0008295; P:spermidine biosynthesis; IEA.
DR GO; GO:0006597; P:spermine biosynthesis; IEA.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 2.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM DCase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
SQ SEQUENCE 434 AA; 49959 MW; 4282D7BF6CCBF209 CRC64;

Query Match 42.0%; Score 890.5; DB 2; Length 434;
Best Local Similarity 44.7%; Pred. No. 1.2e-60;
Matches 193; Conservative 64; Mismatches 114; Indels 61; Gaps 14;

QY 13 YIDHLSATLSDTDAFEGPEKLELWFFPHKKSITTE-KTLRNGMDRWIEILKLVCEV 71
DB 11 YVDHLSANLSDTFAFEGPEKLELWFFPKSENDIPKSEGLRSIPLEKWRVLDLVSKI 70

QY 72 LSMKTKELDAFLSSSLFVFDHKLTKMTCTGTTTLFCKLEKLFQIVEQLSWAFRTQ 131
DB 71 LSMKSKFMFDAYLLSSSLFVFPFKLILTKCTGTTTLACLSELFETVQNV-EG 123

QY 132 ---GKYKPFKVFYRRFCFLPCKQAAIHOWADEVDYLNKFFDNGKSYSGRNDKSNHN 188
DB 124 IDNFDFNVYKIFVRSRSMFPDQKQVHRNKKQEVLLNLYFQNGKSYIVGDTGDDHWY 183

QY 189 LYVTEDTRSPKGEYIEDD--DETEVLMTLDPCEAKSFVCGPEASTTALV-----EP 241
DB 184 LYMGGRD-SVP-SDENANDNVQDTPEILMTLNPEKAENFIADRPKGAESLKESEEE 241

QY 242 NEPKGNLGVQMTNTRLDIYNSAQ-----DSD----- 271
DB 242 EHLGLHDMGQMTCKSKLSDIFPGSNKKLGHSHLPSPSLSDSMELSDDECLKETPTNSD 301

QY 272 -LSFPHDAFAFTPCGYSSNMILAEK--YYVTLHWTPKSGWYASFESNIPVFDISQKQD 328

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DB 302 KFKFIHDAFAFSPCGYSSNSISSNNGGYVYLLHITPESGWSYASFETNYPF--TKDSNES 359
QY 329 NLDVLLHILNVQPRFMSMTFFTKN---YQNSQFQKLSSNESLPD--YTKLQIVYDLD 383
DB 360 IVDLVNKLVDIFQPGKFSVTFITSESDTHDKFNFDLSNCAEDLSEQGYQKQERVLVDLK 419
QY 384 -DYHLFYMKLOK 394
DB 420 FGKLLYLNFTK 431

RESULT 6
Q6C579 PRELIMINARY; PRT; 418 AA.
AC Q6C579;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Similar to tr|Q9Y7F3 Neurospora crassa S-adenosylmethionine
DE decarboxylase.
GN ORFNames=YALIOE20361g;
OS Yarrowia lipolytica CLIB99.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=CLIB99;
RC Genoscope;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382131; CAG79778.1; -
DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
DR GO; GO:0008295; P:spermidine biosynthesis; IEA.
DR GO; GO:0006597; P:spermine biosynthesis; IEA.
DR InterPro; IPR001220; Lectin_legB.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM DCase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
DR PROSITE; PS00307; LECTIN LEGUME BETA; UNKNOWN 1.
SQ SEQUENCE 418 AA; 46500 MW; 9469E694A6F01A5C CRC64;

Query Match 35.7%; Score 756; DB 2; Length 418;
Best Local Similarity 38.5%; Pred. No. 3e-50;
Matches 164; Conservative 68; Mismatches 126; Indels 68; Gaps 10;

QY 12 NYIDHLSATLSDTDAFEGPEKLELWFFPHKKSIT-TEXTLRNGMDRWIEILKLVCE 70
DB 5 HYNHQAIVDLSAEAFEGPEKLELWFAFNQBSLEGTNKSRLNVSTAQWEQLNIVQCK 64

QY 71 VLSMKTKELDAFLSSSLFVFDHKLTKMTCTGTTTLFCKLEKLFQIVEQLSWAFRTQ 130

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Db 65 VLSSVHTSVLDAPVLSSESNMFVPHKLVKCTGTTLLVGIPOKVLBIA-----RTIA 116
QY 131 --CGKTKPKVYFYSRCFLPCKQAAIHONWADEVDYLNKFFDNGKSYSGVRNDKSNHWN 188
Db 117 GFANATPRVYFVSHKTFNCPKQAPPHKSKWDEVSILDSQFNGKAYLVGDTTSDHHWY 176
QY 189 LYVTETD--RSTPKGKEY-IEDDETFEVLMTLDPCEKSFV----- 228
Db 177 CVYTGDDHEEVAHKDHISSHDETWEILMTDLPSSAQFFTDRLPGDANNAGFOHKQ 236
QY 229 -----CGPEASTTALVEPNEDKGNLGYQMTKTRLDIYV 264
Db 237 ELVGVHVVKAFTDTSATSDSGATPACSGTKADP-----GHVLGAYVSTQSGIADIY 292
QY 265 NSAQDSDLGPHHDAFAFTPCGYSSNMILAEKYTYTLHTVTPKGSVSPESNIPVFDISQ 324
Db 293 R-----NKASVAVDSFCFTPCGYANAIVDSGYTYTHVTPQHCVSASFETNVPKAYG- 347
QY 325 GKODNLDVLLHILNVQPREFSMTFTTKYQNSQFQKLLSINBSLPDYIKLDKIVYDLDD 384
Db 348 --MSNIDVIEKVLNVPRPKGLSVTLF--EAENNSLQDCHQFARHLDGKYKTKDKVLYEFDG 403
QY 385 YHLFYM 390
Db 404 YQMVYV 409

RESULT 7

Q9Y7F3 PRELIMINARY; PRT; 503 AA.
AC Q9Y7F3;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE S-adenosylmethionine decarboxylase (EC 4.1.1.50) (Spe-2).
GN Names=Spe-2; Synonyms=B14A6.060;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20309329; PubMed=10852489; DOI=10.1007/s004380051215;
RA Hoyt M.A., Williams-Abbott L.J., Pitkin J.W., Davis R.H.;
RT "Cloning and expression of the S-adenosylmethionine decarboxylase gene
of Neurospora crassa and processing of its product.";
RL Mol. Gen. Genet. 263:664-673 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]

RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF151380; AD34030.1; -
DR EMBL; AL670007; CDD21308.1; -
DR HSSP; P17707; IJL0.
DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008295; P:spermidine biosynthesis; IEA.
DR GO; GO:0006597; P:spermine biosynthesis; IEA.
DR InterPro; IPR00362; Fumarate lyase.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 2.
DR TIGRFAMs; TIGR00535; SAM DCase; 1.
DR PROSITE; PS01336; ADOMETC; 1.
DR PROSITE; PS00163; FUMARATE_LYASES; UNKNOWN_1.
KW Lyase.
SQ SEQUENCE 503 AA; 54721 MW; 4EF83A7BAA2B407B CRC64;

Query Match 32.2%; Score 681; DB 2; Length 503;
Best Local Similarity 32.5%; Pred. NO. 2.5e-44;
Matches 161; Conservative 85; Mismatches 128; Indels 122; Gaps 13;
QY 2 TWIKELTNHVIDHLSATLSDTAPEGPEKLEIWFPPHKSI---TTEKTLRIGMD 58
Db 14 TFSPESGTPLYLTINHDDVAADLSDTAPEGPEKLEIWFPPHKSI---TTEKTLRIGMD 73
QY 59 RTEIILKLVKCEVLSMKTDELDAFLSSSLFVFOHKLTMKTCGTTTTLFCLEKLFQIV 118
Db 74 SWTPMLDLVHCKVLSINSENVDSYLLSSSFVFPFKIILKTCGTTTLLGLDLMRIA 133
QY 119 EDELSSWAFRTQGGK-----YKPFKVFYSRRCFLPCKQAAIHONWADEVDYLNKFFDNG 173
Db 134 AVEAGPPFNVASLEDPKVAATPLRVFYSRKNFLFPQKQRPKHSWRDEVTFLDNMPENG 193
QY 174 KSYSGVRNDKSNHNLVYTETDS-----TPKGKEYIED 207
Db 194 SAYMVGKMN-GDHWLYLTITPTSSLTTPRPTSSRGVSPSRRSKIPTGIVAPFGVIEN 252
QY 208 DDETFEVLMTLDPCEKSFV-----CG----- 230
Db 253 ADETLEILMTDLDPENAKFPYLEEATAIAKEKLFKSEANGDASPDVFSSGDCDAGQA 312
QY 231 --PEASTTALVEPNEDKGNLGYQMTKTRLDIYVNSA-QSDLSLFFHDAFAFTPCGYS 287
Db 313 ILPEALT-----EGHALGTWVSEACGLSAVYPTSTVPDARI---DAYQFSPCGFS 360
QY 288 SNMIL-----AEKYTYTLHTVTPKGSVSPESNIPVFDISQKODNLDVLLHI 336
Db 361 ANGVVPPVAGADGTIPKSGHYFTVHTVTPQCSFASFETNVPG---GQNGRQTAEVIEQV 417
QY 337 LNVFQPREFSMTFF-----TKYQNSQFQKLLSINBSLPDYIKLDKIV 379
Db 418 VNIFFRFSVTLFEAKGALATTPGEDADDSRSGAAAKQRMERIN---GTRVDRIV 473
QY 380 YLDLDYHLYFMKLQKK 395
Db 474 HDFEDYDLVFRYVERE 489

RESULT 8

DCAM SCHPO STANDARD; PRT; 378 AA.
AC Q9P7E3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
DE (SambDC) (Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain).
GN Names=Spe2; ORFNames=SPBP4H10.05c;
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21293067; PubMed=11283013; DOI=10.1074/jbc.M010643200;
RA Chattopadhyay M.K., Murakami Y., Matsufuji S.;
RT "Antizyme regulates the degradation of ornithine decarboxylase in
fission yeast Schizosaccharomyces pombe. Study in the spe2 knockout
strains.";
RL J. Biol. Chem. 276:21235-21241 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jägers K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Mouton L., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skellon J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehtach H., Reinhard R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mortier S.,
RA Galibert F., Aves S.J., Jiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey P., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
RT "The genome sequence of *Schizosaccharomyces pombe*."
RL Nature 415:871-880(2002).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S-deoxy-5-
CC adenosyl)(3-aminopropyl)-methylsulfonium salt + CO(2).
CC -1- COFACTOR: Pyruvoyl group (By similarity).
CC -1- PATHWAY: Decarboxylation of S-adenosylmethionine provides the
CC aminopropyl moiety required for spermidine and spermine
CC biosynthesis from putrescine.
CC -1- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC ENBL; AB045111; BAB12576.1; -.
CC ENBL; AB045110; BAB12575.1; -.
CC ENBL; AL162692; CAB83163.1; -.
CC HSSP; P17707; 1JL0.
CC GeneDB SPombe; SPBP4H10.05c; -.
CC InterPro; IPR001985; SAM decarbox.
CC Pfam; PF01536; SAM decarbox; 1.
CC ProDom; PD002379; SAM decarbox; 2.
CC TIGRFAMs; TIGR00535; SAM_DCase; 1.
CC PROSITE; PS01336; ADOMETDC; 1.
CC Decarboxylase; Lyase; Pyruvate; Spermidine biosynthesis; Zymogen.
CC CHAIN 1 84 S-adenosylmethionine decarboxylase beta
CC FT CHAIN 85 378 S-adenosylmethionine decarboxylase alpha
CC FT CHAIN 85 378 S-adenosylmethionine decarboxylase alpha
CC FT SITE 84 85 Cleavage (nonhydrolytic).
CC FT MOD_RES 85 85 Pyruvic acid (Ser) (By similarity).
CC FT ACT_SITE 21 21 By similarity.
CC FT ACT_SITE 24 24 By similarity.
CC FT ACT_SITE 99 99 By similarity.
CC SQ SEQUENCE 378 AA; 42712 MW; 10AEAB83DAF62894 CRC64;
Query Match 27.0%; Score 571; DB 1; Length 378;
Best Local Similarity 36.0%; Pred. No. 5.8e-36;
Matches 140; Conservative 76; Mismatches 137; Indels 36; Gaps 13;
QY 14 IDHLSATLSDTDAFEGPEKLEIWF-FPHKSIIT-EXT---LRNIGMDRWIEILKLVK 68
Db 7 VDQENSEEF-NTSSFEQPEKLELWFAPIKTNLSAGEKANGLKAVSRNDWDMLAQ 65
QY 69 CEVLSSMKTKELDAFLSSLSVFDHKLTKWTCGTTTLFCLEKLPQIVEQELSWAFRT 128
Db 66 CKVLSSVNSEIDAYLLSSSMFVFAHKIILTKCGTTTLASLPRLLEI-----A 115
QY 129 TGGKYPKPKVYRRRCFLFPCKQAAIHNQWAEVDYLNKFFDNGKSYSGRNDKSNHN 188

Db 116 SSVGFRPLRIFYSRKNFLYPERQLAPHTSWEEVRYLQFFSGCSYVVPINK-NHWH 174
QY 189 LYVTETDRSTPKGEYIEDDETFEVLMTLDEPCASKP-----VCGPEASTALVEP 241
Db 175 LPSDLADDYSL-EDSLDPEDETLEVTMTDMSPEISQFYAPSLDVRSARGDDYVREKN 233
QY 242 NEDKGNLGVQMTKNTLDELIEIYNSAQSDLSPHHDAFAFTPCGYSSNMILAEKYYVTLH 301
Db 234 NLSGGHILSYVADESVDLCTSDKKAVL-----DAFQEPFGFSNMILYKDR-YATIH 288
QY 302 VTPEKGSYASFESNPVDFDISQCKQDNLDVLHLNVFQPREFSTMTFTTKYQNSQFQK 361
Db 289 VTPQHCYSASFETNVSQFGRSISETIE---KTVKTFGANKECLTLFQAGASQ--EK 343
QY 362 LLSIN-ESLPDYIKLKIYVLDLDDYHLFY 389
Db 344 HPSAKLKSPSSYKREBFIVYDFPGYDLIF 372
RESULT 9
DCAM RAT STANDARD; PRT; 333 AA.
ID DCAM RAT AC P17708;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
DE (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-
DE adenosylmethionine decarboxylase beta chain].
OS Name=Amdl;
GN Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90215298; PubMed=2323572; DOI=10.1016/0378-1119(90)90279-2;
RA Pulkka A., Keraenen M.R., Salmela A., Salmikangas P., Ihalaenen R.,
RA Pajunen A.;
RT "Nucleotide sequence of rat S-adenosylmethionine decarboxylase cDNA.
RT Comparison with an intronless rat pseudogene.";
RL Gene 86:193-199(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89034205; PubMed=2460457;
RA Pajunen A., Crozat A., Jaenne O.A., Ihalaenen R., Laitinen P.H.,
RA Stanley B., Madhubala R., Pegg A.E.;
RT "Structure and regulation of mammalian S-adenosylmethionine
RT decarboxylase.";
RL J. Biol. Chem. 263:17040-17049(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92038054; PubMed=1936275; DOI=10.1016/0014-5793(91)81304-Q;
RA Pulkka A., Ihalaenen R., Aatsinki J., Pajunen A.;
RT "Structure and organization of the gene encoding rat S-
RT adenosylmethionine decarboxylase.";
RL FEBS Lett. 291:289-295(1991).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Spleen;
RX MEDLINE=93300506; PubMed=8314573;
RA Pulkka A., Ihalaenen R., Suorsa A., Riviere M., Szpirer J.,
RA Pajunen A.;
RT "Structures and chromosomal localizations of two rat genes encoding S-
RT adenosylmethionine decarboxylase.";
RL Genomics 16:342-349(1993).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S-deoxy-5-
CC adenosyl)(3-aminopropyl)-methylsulfonium salt + CO(2).
CC -1- COFACTOR: Pyruvoyl group.
CC -1- PATHWAY: Decarboxylation of S-adenosylmethionine provides the
CC aminopropyl moiety required for spermidine and spermine
CC biosynthesis from putrescine.

RESULT 10
DCAM MESAU

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Db 108 QSFYKRNKPMKSHQYPRNFQEEIEFLNAPFGAAVCMGRMN-SDCWYLYTLDFPE 166
Qy 197 STPKGEYIEDDETPEVLMTLDPKCAKFKVCGPEASTTALVEPNEDKGNHNLGYQWTKN 256
Db 167 S-----RVINOPDOTLEILMSELDPAVMDQFYM-----KDGVTAKDVIRE 206
Qy 257 TRLDEIYVNSAQSDLSFHHDAFAFTPCGYSNNMILAELKYYTYLHVTPEKGSYASPSN 316
Db 207 SGIRDLPGSVIATL-----FNPCGYSNMGMKSDGTWYTHITPEPEFYSVGFETN 258
Qy 317 IPVPDLSQGDNDLVLHILNVFPQREFSMTFTTKYQNSQFKLSINESLPDYIKLD 376
Db 259 -----LSQTSYD--DLIRKVEVFKGCKFTTLFVN--QSSKRTVLSSPQKIEGFKRLD 309
Qy 377 KIYVDLDYHLFYMKLQK 395
Db 310 CQSAMFNDYNFVFTSPAK 328

RESULT 11
ID DCMI_MOUSE STANDARD; PRT; 334 AA.
AC P31154;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE S-adenosylmethionine decarboxylase proenzyme 1 (BC 4.1.1.50) (AdoMetDC
DE 1) (SamcD 1) [Contains: S-adenosylmethionine decarboxylase 1 alpha
DE chain; S-adenosylmethionine decarboxylase 1 beta chain].
GN Name=Amd1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=93080592; PubMed=149493;
RA Waris T., Ihalaainen R., Keraenen M.-R., Pajunen A.;
RT "Molecular cloning of the mouse S-adenosylmethionine decarboxylase
RT cDNA: specific protein binding to the conserved region of the mRNA 5'-
RT untranslated region.";
RL Biochem. Biophys. Res. Commun. 189:424-429 (1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93345510; PubMed=8344293;
RA Suzuki T., Sadakata Y., Kashiwagi K., Hoshino K., Kakinuma Y.,
RA Shirahata A., Igarashi K.;
RT "Overproduction of S-adenosylmethionine decarboxylase in ethylglyoxal-
RT bis(guanylhydrazonol)-resistant mouse FM3A cells.";
RL Eur. J. Biochem. 215:247-253 (1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ; TISSUE=Spleen;
RX MEDLINE=20035739; PubMed=10570962; DOI=10.1016/S0378-1119(99)00355-8;
RA Nishimura K., Kashiwagi K., Matsuda Y., Jaenne O.A., Igarashi K.;
RT "Gene structure and chromosomal localization of mouse S-
RT adenosylmethionine decarboxylase.";
RL Gene 238:343-350 (1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahy J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -I- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S-deoxy-5-
CC adenosyl) (3-aminopropyl)-methylsulfonium salt + CO(2).
CC -I- COFACTOR: Pyruvoyl group.
CC -I- PATHWAY: Decarboxylation of S-adenosylmethionine provides the
CC aminopropyl moiety required for spermidine and spermine
CC biosynthesis from putrescine.
CC -I- SUBUNIT: Heterotetramer of two alpha and two beta chains (By
CC similarity).
CC -I- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.
CC -----
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CC -----
DR EMBL; Z14986; CAA78710.1; -
DR EMBL; D12780; BAA02243.1; -
DR EMBL; AB025024; BAA83784.1; -
DR EMBL; BC011110; AAH1110.1; -
DR HSP; P17707; IJEN.
DR MGD; MGI:88004; Amd1.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRfam; TIGR00535; SAM_Dcase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
KW Decarboxylase; lyase; Pyruvate; Spermidine biosynthesis; Zymogen.
FT CHAIN 1 67
FT S-adenosylmethionine decarboxylase 1 beta
FT chain.
FT CHAIN 68 334
FT S-adenosylmethionine decarboxylase 1
FT alpha chain.
FT SITE 67 68
FT Cleavage (nonhydrolytic).
FT MOD_RES 68 68
FT Pyruvic acid (Ser).
FT ACT_SITE 8 8
FT By similarity.
FT ACT_SITE 11 11
FT By similarity.
FT ACT_SITE 82 82
FT By similarity.
SQ SEQUENCE 334 AA; 38272 MW; 7950A1E9A9ACBD72 CRC64;

Query Match 22.6%; Score 479; DB 1; Length 334;
Best Local Similarity 30.9%; Pred. No. 6.8e-29;
Matches 117; Conservative 69; Mismatches 137; Indels 56; Gaps 10;

Qy 22 LDSTDAPEGEKLELEWFFPHKKSITT-EKTLNIGMDRWIEILKLVKCVLSMKTKEL 80
Db 1 MEAAHFEETGEKLEWVNFQRQSDASQGSGLRTIPRSEWDVLLKDVQCSIIISVTKDKQ 60
Qy 81 DAFLLSESSLVFDHKLTMKTCGTTTLTFLCEKLQVIEQELSWAFRTTQGGKYKPF--- 137
Db 61 EAVLSESSWVSKRRFILTCTGTTLLKALVPLKLARD-----YSGFDSI 107
Qy 138 -KVYRRRCFLFPCKAAIHQNWAEVDYLNKFPDNGKYSVGRNDSKNHNLVYTETDR 196
Db 108 QSFYKRNKPMKSHQYPRNFQEEIEFLNAPFGAAVCMGRMN-SDCWYLYTLDFPE 166
Qy 197 STPKGEYIEDDETPEVLMTLDPKCAKFKVCGPEASTTALVEPNEDKGNHNLGYQWTKN 256
Db 167 S-----RVINOPDOTLEILMSELDPAVMDQFYM-----KDGVTAKDVIRE 206
Qy 257 TRLDEIYVNSAQSDLSFHHDAFAFTPCGYSNNMILAELKYYTYLHVTPEKGSYASPSN 316
```

TR	TIGRAME;	TIGR00535;	SAM_DCcase; 1.
KW	PROSITE; PS01336;	ADOMETDC; 1.	
DQ	Decarboxylase; Lyase; Pyruvate;	Spermidine biosynthesis; Zymogen.	
FT	CHAIN	1	67 S-adenosylmethionine decarboxylase 2 beta chain.
FT	CHAIN	68	334 S-adenosylmethionine decarboxylase 2 alpha chain.
FT	SITE	67	68 Cleavage (nonhydrolytic).
FT	MOD_RES	68	68 Pyruvic acid (Ser).
FT	ACT_SITE	8	8 By similarity.
FT	ACT_SITE	11	11 By similarity.
FT	ACT_SITE	82	82 By similarity.
FT	MUTAGEN	70	70 I-M: Increases specific activity and proenzyme-processing activity.
SQ	SEQUENCE	334 AA;	38282 MW; A6DFF76F2FC8FA4 CRC64;
Query Match			
Best Local Similarity			
Matches 117; Conservative			
22 LDSTDAFEGPEKLEIWFPFHKSITT-EKTLRNIGMDRWIEILKLVKCEVLSSMKTKEL 80			
::: :::			
Db 1 MEAAHFFEGTEKLELVWFSGQQSDAQSGSGLRTIPRSEWDVLLKDVCQSIIISVTKTDKQ 60			
::: :::			
Qy 81 DAPLSESLFVPDHKLTMKTCGTTTFLCLEKLFQIVEQELSWAFRITOGGKYKPF--- 137			
::: :::			
Db 61 EAYVLSSESI FVRKRPIUKTCTTULLKALVPLLKARD-----YSGFDSI 107			
::: :::			
Qy 138 -KVFSRRCLFPCKQAATHQWAEVDVLYNKFFDNKGYSVGRNOKSHWNLYVTETDR 196			
:::			
Db 108 QSFYRKRFKMFESHQGYPHRNFQEIEFLNLPNGAAYCMGRMN--SDCWLYLTLDPE 166			
:::			
Qy 197 STPKGKEYIEDDETFEVLMTELDPPCASKFVGCPPEASTTALVEPNEDKGHNILGYOMTKN 256			
:::			
Db 167 S-----RVISQPDTLEILMSELDPVAMDQFYM-----KDGVTAKDVRE 206			
::: :::			
Qy 257 TRUDEIVNSAQSDLSFHHDAPAFPTCGSYSSNMILAKEYYYTLHTPKEGWSVASPESN 316			
::: :::			
Db 207 SGIRDLPGSVIDATL-----FNPCGYSMNGMKSDGTYTTHITTPPEFSYVSPETN 258			
::: :::			
Qy 317 IPVFDLSQGDQLNDVLLHLNLNVFQPRESMTFETKNYNQSQFKLLSINESLPDYIKLD 376			
::: :::			
Db 259 -----LSQTSYD--DLIRKVVVFKPGEKFTVTLFVN--QSSKCRTVLSSPQKIDGFKRLD 309			
::: :::			
Qy 377 KIVYDLDYHLFMKLQKK 395			
::: :::			
Db 310 CQSAMENDYNFVTSFAKK 328			
::: :::			
 RESULT 13			
DCM2_MUSSP			
ID	DCM2_MUSSP	STANDARD;	PRT; 334 AA.
AC	P2135;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	25-OCT-2004 (Rel. 45, Last annotation update)		
DE	S-adenosylmethionine decarboxylase proenzyme 2 (EC 4.1.1.50) (AdoMetDC		
DE	2) (SamDC 2) (Contains: S-adenosylmethionine decarboxylase 2 alpha		
DE	chain; S-adenosylmethionine decarboxylase 2 beta chain).		
GN	Name=Amd2;		
OS	Mus spratus (Western wild mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
OX	NCBI_TaxID=10096;		
RN	[1]		
RX	SEQUENCE FROM N.A.		
RC	TISSUE=Liver;		
CC	MEDLINE=99359841; PubMed=10430664;		
RA	Pearson K., Heby O., Berger P.G. ;		
RT	"The functional intronless S-adenosylmethionine decarboxylase gene of		
RT	the mouse (Amd-2) is linked to the ornithine decarboxylase gene (Odc)		
RT	on Chromosome 12 and is present in distantly related species of the		
RT	genus Mus."		

Mamm. Genome 10:784-788 (1999).

CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (5-deoxy-5-adenosyl) (3-aminopropyl)-methylsulfonium salt + CO(2).

CC -1- COFACTOR: Pyruvoyl group (By similarity).

CC -1- PATHWAY: Decarboxylation of S-adenosylmethionine provides the aminopropyl moiety required for spermidine and spermine biosynthesis.

CC -1- SUBUNIT: Heterotrimer of two alpha and two beta chains (By similarity).

CC -1- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.

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DR EMBL; AF052604; AAD45965.1; -.

DR MGD; MG1:1333111; Amd2.

DR InterPro; IPR001985; SAM decarbox.

DR Pfam; PF01536; SAM decarbox; 1.

DR ProDom; PD002379; SAM decarbox; 1.

DR TIGRfams; TIGR00535; SAM_DCase; 1.

DR PROSITE; PS01336; ADOMETDC; 1.

DR Decarboxylase; Lyase; Pyruvate; Spermidine biosynthesis; Zymogen.

CHAIN 1 67 S-adenosylmethionine decarboxylase 2 beta chain.

FT CHAIN 68 334 S-adenosylmethionine decarboxylase 2 alpha chain.

FT SITE 67 68 Cleavage (nonhydrolytic).

FT MOD_RES 68 68 Pyruvic acid (Ser).

FT ACT_SITE 8 8 By similarity.

FT ACT_SITE 11 11 By similarity.

FT ACT_SITE 82 82 By similarity.

FT ACT_SITE 334 334 AA; 3930 MW; A78BB36F2D8134F4 CRC64;

SQ SEQUENCE 334 AA; 3930 MW; A78BB36F2D8134F4 CRC64;

Query Match 22.6%; Score 478; DB 1; Length 334;

Best Local Similarity 30.9%; Pred. No. 8.1e-29;

Matches 117; Conservative 69; Mismatches 137; Indels 56; Gaps 10;

QY 22 LDSTDAFEGEKLELFWFFPKHSITT-EKTLNIGNDRWIEILKLVKCEVLSMKTKEL 80

DB 1 MEAAHFEGETEKLELVWFSRQSDASQSGDLRTIPRSEWDVLLKDVQCSIIISVTKDKQ 60

QY 81 DAFLLSESLFVFDHKLTMKTCGTTTLFCLKLFQIVEQELSWAFRTTQGGYKXP--- 137

DB 61 EAVLSESSNFVSKRRILKTCGTTLLKALVPLKLARD-----YSGFDSI 107

QY 138 -KVFYGRCLFPCKQAIIHONWADEVYLNKFPDNGKYSVGRNDSKSNHNLVYVETDR 196

DB 108 QSFYRKPMKPSHQYPRNFQETEFNLVFPNGAAYCMGRWN-SDCWLYLTLDPE 166

QY 197 STPGKEYIEDDETEFVLTMTLDPKCAKFPVCPPEASTTALVEPNEDKGNLGYQMTKN 256

DB 167 S-----RVISQPDQTLSELSLDPVAVMDQFYM-----KDGVTAKDVIRE 206

QY 257 TRLDIVYVNSAQSDLSFFHDAFAFTPCGYSSNMILAEKYYTYTLHVTPEKWSVASPESN 316

DB 207 SGIRDLIPGSVIDATL-----FNPCCGYSMNGKMSDGTYYWIHTPEPFSVSPETN 258

QY 317 IPVFDISQGGKDNLDVLLHILNVQPREFMTFTFRNQNOSQKLLSINESIPDYIKLD 376

DB 259 -----LSQTSYD--DLIRKVVVEFKPGKFVTTLVFN--QSSKCRITVLSPPQKIDGFKRLD 309

QY 377 KIVYDLDYHLFYMKLOKK 395

DB 310 QCSAMFNDYNFVFTSFAKK 328

DCAM_XENLA STANDARD; PRT; 335 AA.

ID DCAM_XENLA PRT; 335 AA.

AC P79888; 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC) (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain].

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Tail bud;

RC MEDLINE=96328262; PubMed=8765748; DOI=10.1016/0167-4781(96)00020-6;

RA Shinga J., Kashiwagi K., Tashiro K., Igarashi K., Shiohara K.,

RT "Maternal and zygotic expression of mRNA for S-adenosylmethionine decarboxylase and its relevance to the unique polyamine composition in Xenopus oocytes and embryos.";

RT Biochim. Biophys. Acta 1308:31-40(1996).

RL Biochim. Biophys. Acta 1308:31-40(1996).

CC -1- FUNCTION: Involved in the biosynthesis of the polyamines, spermine and spermidine.

CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (5-deoxy-5-adenosyl) (3-aminopropyl)-methylsulfonium salt + CO(2).

CC -1- COFACTOR: Pyruvoyl group.

CC -1- PATHWAY: Polyamines biosynthesis; rate-limiting step.

CC -1- PATHWAY: Decarboxylation of S-adenosylmethionine provides the aminopropyl moiety required for spermidine and spermine biosynthesis from putrescine.

CC -1- DEVELOPMENTAL STAGE: First expressed at stage I of oocyte development, and is maximally expressed at stage II. Levels decline during oocyte maturation and after fertilization, and also in the early neurula. Levels increase dramatically during the late neurula stage reaching a maximum at the tail bud stage.

CC -1- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.

CC -1- CAUTION: It is uncertain whether Met-1 or Met-3 is the initiator.

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CC EMBL; S82621; AAB36519.1; -.

DR PIR; S72197; S72197.

DR HSP; P17707; IJEN.

DR InterPro; IPR001985; SAM decarbox.

DR Pfam; PF01536; SAM decarbox; 1.

DR ProDom; PD002379; SAM decarbox; 1.

DR TIGRfams; TIGR00535; SAM_DCase; 1.

DR PROSITE; PS01336; ADOMETDC; 1.

DR Decarboxylase; Lyase; Polyamine biosynthesis; Pyruvate;

KW Spermidine biosynthesis; Zymogen.

CHAIN 1 69 S-adenosylmethionine decarboxylase beta chain.

FT CHAIN 70 335 S-adenosylmethionine decarboxylase alpha chain.

FT SITE 69 70 Cleavage (nonhydrolytic) (By similarity).

FT MOD_RES 70 70 Pyruvic acid (Ser) (By similarity).

FT ACT_SITE 12 12 By similarity.

FT ACT_SITE 15 15 By similarity.

FT ACT_SITE 84 84 By similarity.

SQ SEQUENCE 335 AA; 36819 MW; BA158A226F21F28C CRC64;

Query Match 22.5%; Score 476; DB 1; Length 335;

Best Local Similarity 31.6%; Pred. No. 1.2e-28;

Matches 118; Conservative 67; Mismatches 127; Indels 62; Gaps 10;

QY 28 FEPEKLELWFPFKHSITTEKTLRNIGMDRWIEILKVKCEVLSMKTKELDAFLSE 87
 Db 11 FEGTEKLELWFSQODAS-KGSGDLRDI PRFWDKLELNVHCLISVTKDKQEAIVLSE 69
 QY 88 SSLFVDPDKLTKMTCTGTTTLFCLEKLFQIVQEQLSWAFRTTGGKYKPF-----KVYFSR 143
 Db 70 SSMFVSKRRFLTKCTGTTLLQALVPLELARE-----YCGFDGIGNFFYSR 116
 QY 144 RCLFPCQAAIHQNAWEDVYLNKFDNGKSYSGRNDKSNHNLVVTETDRSTPKGE 203
 Db 117 KNFKPNKHQYPRHNFHEVEFLNQIPFGAAVCMGRIN-SDCWLYTLTDIP-----DE 169
 QY 204 Y-IEDDDETEVLMTLDPCCASKFCVCGPEASTTALVEPNEDKGNLGYQMTNRLDEI 262
 Db 170 YVISQPDQTLLEILMSLDPVMDQF-----YMKEGVTANDVT 206
 QY 263 YVNSAQSDLSFHHDFAFTPCGYSSNMILAKEYYTLHVTPEKGSYASFPESNIPV--F 320
 Db 207 RVSGIRDLITGVIDATMFPSPCYSGMNGKSDGTGTYTHITPEPDSYVSVFETNLSLTY 266
 QY 321 DISQKQDNLDVLLHILNVFPQREFSMTFTKYNQSFQKLLSINESLDPYIKDKIVY 380
 Db 267 D-----DLISKVDVDFKPKFVTTLFW--QSSKCTTSCAQKIEGFRVRDQFA 315
 QY 381 DLDDYHLFYMKLQK 394
 Db 316 QFNDYNFVFTSAK 329

RESULT 15

DCAM_BOVIN STANDARD; PRT; 334 AA.
 AC P50243;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
 DE (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain].
 GN Name=AMD1;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hill J.R., Morris D.R.;
 RT "Regulation of translation of S-adenosylmethionine decarboxylase mRNA.";
 RL Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 209-232 FROM N.A.
 RX MEDLINE=86304300; PubMed=3017942;
 RA Mach M., White M.W., Neubauer M., Degen J.L., Morris D.R.;
 RT "Isolation of a cDNA clone encoding S-adenosylmethionine decarboxylase. Expression of the gene in mitogen-activated lymphocytes.";
 RT J. Biol. Chem. 261:11697-11703(1986).
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S)-deoxy-5-adenosyl(3-aminopropyl)-methylsulfonium salt + CO(2).
 CC -1- COFACTOR: Pyruvoyl group.
 CC -1- PATHWAY: Decarboxylation of S-adenosylmethionine provides the aminopropyl moiety required for spermidine and spermine biosynthesis from putrescine.
 CC -1- SUBUNIT: Heterotetramer of two alpha and two beta chains (By similarity).
 CC -1- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.
 CC
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CC modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M95605; AAA30359.1; -;
 DR EMBL; M14289; AAA30360.1; -;
 DR PIR; I45851; I45851.
 DR HSSP; P17707; IJEN.
 DR InterPro; IPR001985; SAM decarbox.
 DR Pfam; PF01536; SAM decarbox; 1.
 DR ProDom; PD002379; SAM decarbox; 1.
 DR TIGRFAMs; TIGR00535; SAM DCbase; 1.
 DR PROSITE; PS01336; ADOMETDC; 1.
 KW Decarboxylase; Lyase; Pyruvate; Spermidine biosynthesis; Zymogen.
 FT CHAIN 1 67 S-adenosylmethionine decarboxylase beta chain.
 FT CHAIN 68 334 S-adenosylmethionine decarboxylase alpha chain.
 FT SITE 67 68 Cleavage (nonhydrolytic).
 FT MOD_RES 68 68 Pyruvic acid (Ser).
 FT ACT_SITE 8 8 Important for catalytic activity (By similarity).
 FT ACT_SITE 11 11 Important for catalytic activity (By similarity).
 FT ACT_SITE 82 82 Important for catalytic activity (By similarity).
 SQ SEQUENCE 334 AA; 38364 MW; D8AFB98C9D8DA1E9 CRC64;

Query Match 22.3%; Score 473; DB 1; Length 334;

Best Local Similarity 30.6%; Pred. No. 2e-28;

Matches 116; Conservative 69; Mismatches 138; Indels 56; Gaps 10;

QY 22 LDSTAFEGPEKLELWFPFKHSITT-EKTLRNIGMDRWIEILKVKCEVLSMKTKEL 80
 Db 1 MEAHFEGTEKLELWFSRQDPDANQSGDLRTIPSEWDILLKDVQCSIIIVTKDKQ 60
 QY 81 DAPLSESLFVDPDKLTKMTCTGTTTLFCLEKLFQIVQEQLSWAFRTTGGKYKPF--- 137
 Db 61 EAVLSESSMFVSKRRFILKTCGTTLLKALVPLLLARD-----YSGFDSI 107
 QY 138 -KVYFSRRCFLPCKQAAIHQNAWEDVYLNKFDNGKSYSGRNDKSNHNLVVTETDR 196
 Db 108 QSEFFSKRNFMPKPSHQGYPRHNFQEEIFLNALFPNGAAYCMGRMN-SDCWLYTLDPPE 166
 QY 197 STPKGEYIEDDDTEPEVLMTLDPCCASKFCVCGPEASTTALVEPNEDKGNLGYQMTKN 256
 Db 167 S-----RVINQPDQTLLEILMSLDPVMDQFYM-----KGVTAQDVRE 206
 QY 257 TRLDEIYVNSAQSDLSFHHDFAFTPCGYSSNMILAKEYYTLHVTPEKGSYASFPESN 316
 Db 207 SGIRDLIPGSVIDATM-----FNPCGYSMNGKSDGTGTYTHITPEPDSYVSPETN 258
 QY 317 IPVFDISQKQDNLDVLLHILNVFPQREFSMTFTKYNQSFQKLLSINESLDPYIKLD 376
 Db 259 -----LSQTSYD--DLIRKVVVEFKGFKFVTTLFWN--QSSKCTTSLSPQKIEGFKRLD 309
 QY 377 KIVYDLDYHLFYMKLQK 395
 Db 310 CQSALFNDINFTVFTSAK 328

Search completed: May 11, 2005, 22:52:28

Job time : 96.5567 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 11, 2005, 22:42:53 ; Search time 21.3058 Seconds
(without alignments)
1806.392 Million cell updates/sec

Title: US-10-732-923-408

Perfect score: 2097

Sequence: 1 MAVLSAADASPVSAIGFEGY.....LLCWEEDAMEEKAGVLDE 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2097	100.0	400	2 T03947	adenosylmethionine
2	1682.5	80.2	393	2 S69191	adenosylmethionine
3	1657	79.0	398	2 T04099	adenosylmethionine
4	980	46.7	357	2 S68990	adenosylmethionine
5	971	46.3	361	2 T01934	adenosylmethionine
6	961.5	45.9	363	2 S49222	adenosylmethionine
7	954	45.5	377	2 T10708	adenosylmethionine
8	951.5	45.4	360	2 S52662	adenosylmethionine
9	946.5	45.1	353	2 T06515	probable adenosylm
10	944	45.0	381	2 T10707	adenosylmethionine
11	879	41.9	361	2 T12613	adenosylmethionine
12	874.5	41.7	369	2 T10750	probable adenosylm
13	869.5	41.5	362	2 T51378	adenosylmethionine
14	466	22.2	368	2 T22361	adenosylmethionine
15	423	20.2	334	1 DCHYDM	adenosylmethionine
16	420	20.0	334	1 DCHUDM	adenosylmethionine
17	420	20.0	334	2 A55948	adenosylmethionine
18	415	19.8	333	1 DCRTDM	adenosylmethionine
19	396	18.9	335	2 S72197	adenosylmethionine
20	372.5	17.8	396	1 DCBYDM	adenosylmethionine
21	108.5	5.2	530	2 S65773	glutamyi-trna redu
22	108.5	5.2	530	2 G86233	hypothetical prote
23	100	4.8	603	2 G82738	gamma-glutamyltran
24	96.5	4.6	410	2 AH3376	glycosyltransferas
25	96	4.6	593	2 S65470	pyruvate decarboxy
26	95.5	4.6	1307	2 T35944	probable beta-gala
27	94	4.5	1165	2 S11446	parasporal crystal
28	92	4.4	689	2 F81286	probable polysacch
29	91.5	4.4	560	2 B86661	hypothetical prote

oxoglutarate dehyd
nitrite reductase
LDL-receptor-relat
rf2 nuclear reator
glutamate synthase
alcohol dehydrogen
DNA helicase homol
hypothetical prote
hypothetical prote
hypothetical prote
nitrite reductase
N-acetylornithine
beta-N-acetylhexos
glycine cleavage s
polygalacturonase
hypothetical prote

ALIGNMENTS

RESULT 1
T03947
adenosylmethionine decarboxylase (EC 4.1.1.50) - maize
N;Alternate names: S-adenosylmethionine decarboxylase
C;Species: Zea mays (maize)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T03947
R;Michael, A.J.
submitted to the EMBL Data Library, September 1996
A;Reference number: Z15155
A;Accession: T03947
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-400 <MC>
A;Cross-references: UNIPROT:O24575; EMBL:Y07767; PIDN:CAA69075.1
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
P;78/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 100.0%; Score 2097; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 4.5e-170;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAVLSAADASPVSAIGFEGYKRLITFSEAPVFDPHGRGLRALGRAQIDSVLDLARCT	60
DB	1	MAVLSAADASPVSAIGFEGYKRLITFSEAPVFDPHGRGLRALGRAQIDSVLDLARCT	60
QY	61	IVSELSNKDFDSVLSSESLFIYPLKIVIKTCGTTKLLLTIPRILELAELSMLAAVKY	120
DB	61	IVSELSNKDFDSVLSSESLFIYPLKIVIKTCGTTKLLLTIPRILELAELSMLAAVKY	120
QY	121	SRGTFFPGAQAPAPHRFSFEVVAALNRYFGGLKSGGNAYVIGDPAPGQKWHFYATEYP	180
DB	121	SRGTFFPGAQAPAPHRFSFEVVAALNRYFGGLKSGGNAYVIGDPAPGQKWHFYATEYP	180
QY	181	EQPMVNLWCMTGLDKKACVFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDPEPC	240
DB	181	EQPMVNLWCMTGLDKKACVFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDPEPC	240
QY	241	GYSMNAIHGSAFSTIHTVTPEDGFSYASVEVMGLDATALSYGLDKRVLRCFGPSEFSVAV	300
DB	241	GYSMNAIHGSAFSTIHTVTPEDGFSYASVEVMGLDATALSYGLDKRVLRCFGPSEFSVAV	300
QY	301	TIFGGRGHAGTWGKALGAEVYDCNNVVEQLPGGGLLVYQSFCAAEADAVATSPKSPFHCF	360
DB	301	TIFGGRGHAGTWGKALGAEVYDCNNVVEQLPGGGLLVYQSFCAAEADAVATSPKSPFHCF	360
QY	361	DGENVESAPPPMKDKYKLANLLCWEEDAMEEKAGVLDE	400
DB	361	DGENVESAPPPMKDKYKLANLLCWEEDAMEEKAGVLDE	400

RESULT 2

S69191
adenosylmethionine decarboxylase (EC 4.1.1.50) precursor - wild barley
C;Species: Hordeum chilense (wild barley)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S69191
R;Dresselhaus, T.; Barcelo, P.; Hagel, C.; Loerz, H.; Humbeck, K.
Plant Mol. Biol. 30, 1021-1033, 1996
A;Title: Isolation and characterization of a Tritordeum cDNA encoding S-adenosylmethionine decarboxylase
A;Reference number: S69191; MUID:96270379; PMID:8639739
A;Accession: S69191
A;Molecule type: mRNA
A;Residues: 1-393 <DRE>
A;Cross-references: UNIPROT:Q42829; EMBL:X83881; NID:g1403043; PIDN:CAA58762.1; PID:g1403043
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; eukaryotic type
F;1-71/Product: adenosylmethionine decarboxylase beta chain #status predicted <MAT1>
F;72-393/Product: adenosylmethionine decarboxylase alpha chain #status predicted <MAT2>
F;247-262/Region: PEST sequence
F;71/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match	80.2%;	Score 1682.5;	DB 2;	Length 393;	
Best Local Similarity	82.7%;	Pred. No. 6.6e-135;			
Matches	324;	Conservative 25;	Mismatches 38;	Indels 5;	Gaps 3;

QY	9	ASPVS	AI	GF	EG	YK	RL	ET	FS	EA	VP	VD	PH	GR	GL	R	A	L	S	R	A	Q	I	D	S	V	L	D	L	A	R	C	T	I	V	S	E	L	S	N	K	68												
DB	2	AAPV	SA	IG	FE	GE	YK	RL	ET	FS	EA	VP	VD	PH	GR	GL	R	A	L	S	R	A	Q	I	D	S	V	L	D	L	A	R	C	T	I	V	S	E	L	S	N	K	61											
QY	69	DPDS	YV	LS	SS	SL	PI	YK	VI	KT	CG	TT	KL	LT	TP	RI	LE	A	E	L	S	M	P	L	A	A	V	K	Y	S	R	G	T	I	P	P	128																	
DB	62	DPDS	YV	LS	SS	SL	PI	YK	VI	KT	CG	TT	KL	LT	TP	RI	LE	A	E	L	S	M	P	L	A	A	V	K	Y	S	R	G	T	I	P	P	121																	
QY	129	GQAP	PH	RS	FE	SE	VA	AL	NR	YF	GL	K	S	G	N	A	Y	V	I	G	D	P	A	R	P	G	K	W	H	V	F	A	T	E	Y	P	188																	
DB	122	GQAP	PH	RS	FE	SE	VA	AL	NR	YF	GL	K	S	G	N	A	Y	V	I	G	D	P	A	R	P	G	K	W	H	V	F	A	T	E	Y	P	181																	
QY	189	MCMT	GL	DK	KA	CV	FF	KT	AD	GN	TT	CA	K	E	M	T	K	L	S	G	I	S	E	I	P	E	M	E	I	C	D	F	P	E	C	P	248																	
DB	182	MCMT	GL	DK	KA	CV	FF	KT	AD	GN	TT	CA	K	E	M	T	K	L	S	G	I	S	E	I	P	E	M	E	I	C	D	F	P	E	C	P	241																	
QY	249	GS	AF	ST	I	H	V	T	P	E	D	G	F	S	Y	A	S	Y	E	V	M	G	L	D	A	T	A	L	S	Y	G	D	L	V	K	R	V	L	R	C	F	G	S	E	F	S	V	A	V	308				
DB	242	GS	AF	ST	I	H	V	T	P	E	D	G	F	S	Y	A	S	Y	E	V	M	G	L	D	A	T	A	L	S	Y	G	D	L	V	K	R	V	L	R	C	F	G	S	E	F	S	V	A	V	301				
QY	309	AG	T	W	K	A	L	G	A	E	V	Y	D	C	N	N	V	E	Q	E	L	P	G	G	L	I	Y	Q	S	F	A	E	D	A	V	--	A	T	S	P	K	S	V	F	H	C	F	D	G	E	N	V	E	366
DB	302	AAT	W	K	K	L	D	A	E	Y	D	C	N	N	V	E	Q	E	L	P	G	G	L	I	Y	Q	S	F	A	E	D	A	V	--	A	T	S	P	K	S	V	F	H	C	F	D	G	E	N	V	E	359		
QY	367	S	A	P	P	P	K	K	D	Y	K	L	A	N	L	C	W	E	E	E	A	D	A	M	E	E	K	A	G	V	L	398																						
DB	360	S	G	-	H	P	L	V	K	E	G	K	L	A	N	L	A	R	A	E	E	S	L	E	B	E	G	T	G	A	L	390																						

RESULT 3

T04099
adenosylmethionine decarboxylase homolog [similarity] - rice
C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Mar-2004
R;Accession: T04099
R;Michael, A.J.
submitted to the EMBL Data Library, September 1996
A;Description: Spermidine biosynthesis in rice.
A;Reference number: Z15210
A;Accession: T04099
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-398 <MIC>
A;Cross-references: EMBL:Y07766; PIDN:CAA69074.1
A;Experimental source: cv. Nipponbare
A;Note: this sequence appears to lack the residues necessary to form an active site
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type

Query Match	79.0%;	Score 1657;	DB 2;	Length 398;	
Best Local Similarity	80.8%;	Pred. No. 9.8e-133;			
Matches	325;	Conservative 23;	Mismatches 48;	Indels 6;	Gaps 4;

QY	1	MAV	L	S	A	A	D	A	S	P	V	S	A	I	G	F	E	G	Y	K	R	L	E	I	T	F	S	E	A	P	V	F	D	P	H	G	R	G	L	R	A	L	S	R	A	Q	I	D	S	V	L	D	L	A	R	C	T	60				
DB	1	M	G	D	L	S	A	A	D	P	P	P	V	S	A	I	G	F	E	G	Y	K	R	L	E	I	T	F	S	E	A	P	V	F	D	P	H	G	R	G	L	R	A	L	S	R	A	Q	I	D	S	V	L	D	L	A	R	C	T	60		
QY	61	I	V	S	E	L	S	N	K	D	F	S	Y	L	S	S	S	L	F	I	P	L	K	I	V	I	K	T	C	G	T	T	K	L	L	T	I	P	R	I	L	E	A	E	L	S	M	P	L	A	A	V	K	Y	120							
DB	61	I	V	S	E	L	S	N	K	D	F	S	Y	L	S	S	S	L	F	I	P	L	K	I	V	I	K	T	C	G	T	T	K	L	L	T	I	P	R	I	L	E	A	E	L	S	M	P	L	A	A	V	K	Y	120							
QY	121	S	R	G	T	F	I	P	G	A	P	H	R	S	F	S	E	E	V	A	L	N	R	Y	F	G	L	K	S	G	N	A	Y	V	I	G	D	P	A	R	P	G	K	W	H	V	F	A	T	E	Y	P	180									
DB	121	S	R	G	M	F	I	P	G	A	P	H	R	S	F	S	E	E	V	A	L	N	R	Y	F	G	L	K	S	G	N	A	Y	V	I	G	D	P	A	R	P	G	K	W	H	V	F	A	T	E	Y	P	180									
QY	181	E	O	P	M	N	L	E	M	C	M	T	G	L	D	K	K	A	C	V	F	F	K	T	N	A	D	G	N	T	T	C	A	K	E	M	T	K	L	S	G	I	S	E	I	P	E	M	E	I	C	D	F	P	E	C	240					
DB	181	E	O	P	M	V	T	L	E	M	C	M	T	G	L	D	K	E	K	A	S	V	F	F	K	T	S	A	D	G	H	T	S	C	A	K	E	M	T	K	L	S	G	I	S	D	I	P	E	M	E	I	C	D	F	P	E	C	240			
QY	241	G	Y	S	M	N	A	I	H	G	S	A	F	S	T	I	H	V	T	P	E	D	G	F	S	Y	A	S	Y	E	V	M	G	L	D	A	T	A	L	S	Y	G	D	L	V	K	R	V	L	R	C	F	G	S	E	F	S	V	A	V	300	
DB	241	G	Y	S	M	N	A	I	H	G	S	A	F	S	T	I	H	V	T	P	E	D	G	F	S	Y	A	S	Y	E	V	M	G	L	D	A	T	A	L	S	Y	G	D	L	V	K	R	V	L	R	C	F	G	S	E	F	S	V	A	V	300	
QY	301	T	I	F	G	G	H	A	G	T	W	A	K	E	L	N	A	D	A	Y	K	C	N	N	V	E	Q	E	L	P	G	G	L	I	Y	Q	S	F	A	E	D	A	V	--	A	T	S	P	K	S	V	F	H	C	F	D	G	E	N	V	E	358
DB	301	T	I	F	G	G	H	A	G	T	W	A	K	E	L	N	A	D	A	Y	K	C	N	N	V	E	Q	E	L	P	G	G	L	I	Y	Q	S	F	A	E	D	A	V	--	A	T	S	P	K	S	V	F	H	C	F	D	G	E	N	V	E	360
QY	359	C	F	D	G	E	N	V	E	S	A	P	P	P	K	K	D	Y	K	L	A	N	L	C	W	E	E	E	A	D	A	M	E	E	K	A	G	V	L	D	E	400																				
DB	361	C	F	E	A	E	N	M	V	-	P	A	P	V	K	E	G	-	K	L	G	N	L	L	P	W	G	E	--	D	A	L	E	N	D	G	V	F	D	E	398																					

RESULT 4

S68990
adenosylmethionine decarboxylase (EC 4.1.1.50) - Madagascar periwinkle
N;Alternate names: S-adenosyl-L-methionine decarboxylase proenzyme
C;Species: Catharanthus roseus (Madagascar periwinkle)
C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: S68990
R;Schroeder, G.; Schroeder, J.
Eur. J. Biochem. 228, 74-78, 1995
A;Title: cDNAs for S-adenosyl-L-methionine decarboxylase from Catharanthus roseus, heterologous to the active enzyme, and a conserved region in the 5' mRNA leader.
A;Reference number: S68989; MUID:95188916; PMID:7883014
A;Accession: S68990
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-357 <SCH>
A;Cross-references: UNIPROT:Q42679; EMBL:U12573; NID:g758693; PID:g758695
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;71/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match	46.7%;	Score 980;	DB 2;	Length 357;	
Best Local Similarity	51.6%;	Pred. No. 2.4e-75;			
Matches	204;	Conservative 56;	Mismatches 87;	Indels 48;	Gaps 8;

QY	9	ASP	V	S	A	I	G	F	E	G	Y	K	R	L	E	I	T	F	S	E	A	P	V	F	D	P	H	G	R	G	L	R	A	L	S	R	A	Q	I	D	S	V	L	D	L	A	R	C	T	I	V	S	E	L	S	N	K	68
DB	2	ALP	AS	A	I	G	F	E	G	Y	K	R	L	E	I	S	F	F	S	S	F	P	A	D	P	D	G	K	L	R	A	L	N	K	S	I	D	E	I	L	E	A	E	I	P	A	E	C	T	I	V	D	S	L	S	N	Q	61
QY	69	D	F	S	Y	V	L	S	S	S	L	F	I	P	L	K	I	V	I	K	T	C	G	T	T	K	L	L	T	I	P	R	I	L	E	A	E	L	S	M	P	L	A	A	V	K	Y	S	R	G	T	I	P	P	128			
DB	62	Y	L	D	S	Y	V	L	S	S	S	L	F	I	P	L	K	I	V	I	K	T	C	G	T	T	K	L	L	T	I	P	R	I	L	E	A	E	L	S	M	P	L	A	A	V	K	Y	S	R	G	T	I	P	P	121		
QY	129	G	Q	A	P	H	R	S	F	S	E	V	A	L	N	R	Y	F	G	L	K	S	G	N	A	Y	V	I	G	D	P	A	R	P	G	K	W	H	V	F	A	T	E	Y	P	Q	--	P	M	V	185							
DB	122	G	A	O	S	F	P	H	R	S	F	S	E	V	E	L	L	D	N	F	G	L	G	E	S	N	A	F	I	M	G	N	F	D	Q	--	O	K	W	H	V	I	S	A	S	V	G	S	Q	S	S	D	T	Y	180			
QY	186	N	L	E	M	C	M	T	G	L	D	K	K	A	C	V	F	F	K	T	N	A	D	G	N	T	T	C	A	K	E	M	T	K	L	S	G	I	S	E	I	P	E	M	E	I	C	D	F	P	E	C	G	Y	S	M	N	245
DB	181	T	L	E	M	C	M	T	G	L	D	R	E	K	A	S	V	F	Y	K	S	---	E	S	S	A	L	M	T	T	R	S	G	I	R	K	I	L	P	D	S	E	I	C	D	F	E	P	C	G	Y	S	M	N	236			

A;Description: A spinach cDNA with homology to S-adenosylmethionine decarboxylase.

A;Reference number: S49222

A;Accession: S49222

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-363 <BOL>

A;Cross-references: UNIPROT:P46255; EMBL:X81414; NID:g547471; PID:g547472

C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type

C;Keywords: Blocked amino end; carbon-carbon lyase; carboxy-lyase

F;69/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 45.9%; Score 961.5; DB 2; Length 363;
Best Local Similarity 51.5%; Pred.No.9.2e-74;
Matches 204; Conservative 49; Mismatches 92; Indels 51; Gaps 10;

QY 12 VSAIGFEGEKRLIEITFSBPVFDPHGRGLRALSRAQIDSVLDLARCTIVSLSNKNDFD 71
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 3 ISAIGFEGFEKRLIEITFPSIFVDPEGKLRAQLDEILGPAECTIVDSLAVESVD 62

QY 72 SYVLSSSLFIYPLKVIKITCGTTKLLLIPIRILELAELSMPAAVKYSRGTFIFPGAQ 131
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 63 SYVLSSSLFIYAYKIIIKTCGTTKLLRAIPTLRILAGKSLDKSVRYTRGSFIFPGAQ 122

QY 132 PAPHRSFSEVALNRYPFGLSGGNAYVGDPARGQKHVFYATETP---EOPMVNL 188
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 123 SVAHRSFSEVALVDGYFKLAGSAKFVNGDPAKP-QRWHVYSAGAETISPEEPVTTL 181

QY 189 MCMTGLDKKKACVFFFTKTADGNNTTCAKEMTKLSGISIIPMEICDFDFEPCGYSMAIH 248
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 182 MCMTGLKKEKASVFFKSQSPN---AAMTESSGIRKIPLDSKICDFDFEPCGYSMAIE 237

QY 249 GSASFSTHTPTPDGFSYASYEVWGLDATALSYGDVLKRVLCRFGPSSEFSVAVTIFGGRGH 308
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 238 GPAISTHITPTPDGFSYAFVGVYDKKLTDLNQLVERVLACFEPSEFSIAI-----H 290

QY 309 AGTWGAKALAEVY-DQNNVVEQLPGGL-----LVYQSFCFAEDAVATSPKSVFH 358
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 291 AETAANSMEHCNVNNGYSREE--GGTEELGFGAASVYQKFCASTGFGATNK---- 343

QY 359 CPGDENVESAPPMMKYDKLANLLCWEEBADAMEEK 394
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 344 -----PPALK-----CCWKE--DKFEEE 360

RESULT 7
T10708
adenosylmethionine decarboxylase (EC 4.1.1.50) 2 - clove pink
N;Alternate names: S-adenosylmethionine decarboxylase 2
C;Species: Dianthus caryophyllus (Clove pink)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10708
R;Lee, M.M.; Lee, S.H.; Park, K.Y.
submitted to the EMBL Data Library, October 1995
A;Description: Nucleotide sequence of cDNAs encoding S-adenosylmethionine decarboxylase
A;Reference number: Z17089
A;Accession: T10708
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-377 <LEE>
A;Cross-references: UNIPROT:Q39677; EMBL:U38527; NID:gl155241; PID:gl155242
A;Experimental source: cv. White Sim; carnation petal
C;Function:
A;Description: catalyzes the decarboxylation of S-adenosyl-L-methionine to (S-deoxy-S-ac
A;Pathway: polyamine biosynthesis
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: Blocked amino end; carbon-carbon lyase; carboxy-lyase
F;84/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 45.5%; Score 954; DB 2; Length 377;
Best Local Similarity 52.7%; Pred.No.4.2e-73;
Matches 205; Conservative 47; Mismatches 87; Indels 50; Gaps 11;

QY 12 VSAIGFEGEKRLIEITFSBPVFDPHGRGLRALSRAQIDSVLDLARCTIVSLSNKNDF 71

18 ISAIPEGKRLLEISFFEPGIFVDPGKGLRALSKAHLDEILGPAECTIVDSLANESVD 77
72 SYVLSSSLFIYPLKVIKTCGTTKLLTIPRILELAELSMPAAVKYSGRTFIFPGAQ 131
78 SYVLSSSLFVYSYKIIKTCGTTKLLNSIPILRLAETLFLDVKSRYTRGSFIFPGAQ 137
132 PAPHRFSSEVAALNRYFGLKSGGNAYVIGDPAFCQKWHVYATEYP--EOPMVNLEM 189
138 SPHRFSSEVAALNRYFGLKSGGNAYVIGDPAFCQKWHVYATEYP--EOPMVNLEM 196
190 CMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFDFEPCGYSMAIHG 249
197 CMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFDFEPCGYSMAIHG 252
250 SAFSTIHTVTPEDGFSYASVEVMGLDATALSYGDLVLRVLCRFGPSEFSVAVTIFGGRGHA 309
253 PAVSTIHTVTPEDGFSYASVEVMGLDATALSYGDLVLRVLCRFGPSEFSVAVTIFGGRGHA 309
310 --GTWKGALCAEVYDCN--NMVE-----QELPGGGLLVYQSCFAEDAVATSPKSVFH 358
306 DTDADTKVLAR--NCSVNVIYSGREEGIEELGSGVYQKFC--GTAP----- 352
359 CPGENVESAPPMKKDYKLANLLCWEEERADAMEEKAG 396
353 -----VCPAPKTKL-----CCWKEE 369

RESULT 8
S52662
adenosylmethionine decarboxylase (EC 4.1.1.50) TUB13 [similarity] - potato
C;Species: Solanum tuberosum (potato)
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
R;Accession: S52662; S28047
R;Arif, S.A.M.; Taylor, M.A.; George, L.A.; Butler, A.R.; Burch, L.R.; Davies, H.V.; Sta
plant Mol. Biol. 26: 327-338, 1994
A;Title: Characterisation of the S-adenosylmethionine decarboxylase (SAMDC) gene of pota
A;Reference number: S52662; MUID:95036004; PMID:7948879
A;Accession: S52662
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-360 <ARI>
A;Cross-references: UNIPROT:Q04694; GB:S74514; NID:9807093; PIDN:AAB32507.1; PID:9807094
R;Taylor, M.A.; Arif, S.A.M.; Kumar, A.; Davies, H.V.; Scobie, L.A.; Pearce, S.R.; Flav
Plant Mol. Biol. 20: 641-651, 1992
A;Title: Expression and sequence analysis of cDNAs induced during the early stages of tu
A;Reference number: S28046; MUID:93081725; PMID:1450379
A;Accession: S28047
A;Molecule type: mRNA
A;Residues: 1-173, 'S', 175-256, 'T', 258-290, 'V', 292-304, 'I', 306-360 <TAY>
A;Cross-references: EMBL:Z11680; GB:S51455; NID:G21484; PIDN:CAA77742.1; PID:G21485
C;Genetics:
A;Gene: TUB13
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;73/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 45.4%; Score 951.5; DB 2; Length 360;
Best Local Similarity 51.4%; Pred. No. 6.5e-73;
Matches 203; Conservative 47; Mismatches 94; Indels 51; Gaps 8;

11 PVSAIFEGEYKRLLEISFFEPGIFVDPGKGLRALSKAHLDEILGPAECTIVDSLANESVD 70
6 PVSAIFEGEYKRLLEISFFEPGIFVDPGKGLRALSKAHLDEILGPAECTIVDSLANESVD 65
71 DSVLSSSLFIYPLKVIKTCGTTKLLTIPRILELAELSMPAAVKYSGRTFIFPGA 130
66 DSVLSSSLFVYSYKIIKTCGTTKLLNSIPILRLAETLFLDVKSRYTRGSFIFPGA 125
131 QPAPHRFSSEVAALNRYFGLKSGGNAYVIGDPAFCQKWHVYATEYPEQ---PMVNL 187
126 QSPHRFSSEVAALNRYFGLKSGGNAYVIGDPAFCQKWHVYATEYPEQ---PMVNL 184

188 EMCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFDFEPCGYSMAI 247
185 EMCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFDFEPCGYSMAI 240
248 HGSASFSTIHTVTPEDGFSYASVEVMGLDATALSYGDLVLRVLCRFGPSEFSVAVTIFGGRG 307
241 EGAAVSTIHTVTPEDGFSYASVEVMGLDATALSYGDLVLRVLCRFGPSEFSVAVTIFGGRG 293
308 HAGTWKGALCAEVYDCN--NMVE-----QELPGGGLLVYQSCFAEDAVATSPKSVFHCFD 361
294 HADVATKLLERTCSDVDVKGYSALWSPSEFEGGSIYQKFC--TRTPYCSPPKSVLKG-- 349
362 GENVESAPPMKKDYKLANLLCWEEERADAMEEKAG 396
350 -----CWKE-----EKEKG 358

RESULT 9
T06515
probable adenosylmethionine decarboxylase (EC 4.1.1.50) - garden pea
C;Species: Pisum sativum (garden pea)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T06515
R;Carrasco, P.; Marco, F.
submitted to the EMBL Data Library, June 1996
A;Description: Pea S-adenosylmethionine decarboxylase.
A;Reference number: Z15729
A;Accession: T06515
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-353 <CAR>
A;Cross-references: UNIPROT:Q43820; EMBL:U60592; NID:G1421750; PIDN:AAB03865.1; PID:G1421
A;Experimental source: cv. Alaska
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;69/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 45.1%; Score 946.5; DB 2; Length 353;
Best Local Similarity 53.9%; Pred. No. 1.7e-72;
Matches 193; Conservative 56; Mismatches 98; Indels 11; Gaps 5;

12 VSAIFEGEYKRLLEISFFEPGIFVDPGKGLRALSKAHLDEILGPAECTIVDSLANESVD 71
3 VSAIFEGEYKRLLEISFFEPGIFVDPGKGLRALSKAHLDEILGPAECTIVDSLANESVD 62
72 SYVLSSSLFIYPLKVIKTCGTTKLLTIPRILELAELSMPAAVKYSGRTFIFPGAQ 131
63 SYVLSSSLFVYSYKIIKTCGTTKLLNSIPILRLAETLFLDVKSRYTRGSFIFPGAQ 122
132 PAPHRFSSEVAALNRYFGLKSGGNAYVIGDPAFCQKWHVYATE---YEPQMVNLE 188
123 SPHRFSSEVAALNRYFGLKSGGNAYVIGDPAFCQKWHVYATE---YEPQMVNLE 181
189 MCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFDFEPCGYSMAI 248
182 MCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFDFEPCGYSMAI 237
249 GSASFSTIHTVTPEDGFSYASVEVMGLDATALSYGDLVLRVLCRFGPSEFSVAVTIFGGRGH 308
238 GSAVSTIHTVTPEDGFSYASVEVMGLDATALSYGDLVLRVLCRFGPSEFSVAVTIFGGRGH 296
309 AGTWKGALCAEVYDCN--NMVE-----QELPGGGLLVYQSCFAEDAVATSPKSVFHCFDGENVE 366
297 SFEQGLLDVKGVCCEKSHQGLMGSGVYQKFC--LKTSYCGSPRSTLCKWDEDEE 352

RESULT 10
T10707
adenosylmethionine decarboxylase (EC 4.1.1.50) 1 - clove pink
N;Alternate names: S-adenosylmethionine decarboxylase 1
C;Species: Dianthus caryophyllus (clove pink)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10707; T10787

R;Lee, M.M.; Lee, S.H.; Park, K.Y.
submitted to the EMBL Data Library, October 1995
A;Description: Nucleotide sequence of cDNAs encoding S-adenosylmethionine decarboxylase
A;Reference number: Z17089
A;Accession: T10707
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-381 <LEE>
A;Cross-references: UNIPROT:Q39676; EMBL:U38526; NID:g1155239; PID:g1155240
A;Experimental source: cv. White Sim; carnation petal
R;Kim, Y.J.; Lee, M.M.; Chang, K.S.; Lee, S.H.; Park, K.Y.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z17144
A;Accession: T10787
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-381 <KIM>
A;Cross-references: EMBL:U94786; NID:g2406584; PID:g2406585
A;Experimental source: strain White sim
A;Genetics:
A;Gene: gscd39
C;Function:
A;Description: catalyzes the decarboxylation of S-adenosyl-L-methionine to (S)-deoxy-5-adenosylmethionine
A;Pathway: polyamine biosynthesis
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;93/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 45.08; Score 944; DB 2; Length 381;
Best Local Similarity 55.54; Pred. No. 3e-72;
Matches 197; Conservative 48; Mismatches 84; Indels 26; Gaps 7;

QY 12 VSAIGEGYKRLIEITPSEAPVFDPHGRGLRALSRQAIDSVDLRLARCTIVSELSNKKDFD 71
DB 27 LSAIGEGYKRLIEITPSEAPVFDPHGRGLRALSRQAIDSVDLRLARCTIVSELSNKKDFD 86
QY 72 SYLVSESLFIYPLKIVIKTCGTTKLLTTPRIELAEELSMPAAVYKSGRTFFPGAQ 131
DB 87 SYLVSESLFIYPLKIVIKTCGTTKLLTTPRIELAEELSMPAAVYKSGRTFFPGAQ 146
QY 132 PAHRSESEVAALNRYFGGLKSGGNAYVIGDPAKQKWHVYATYEP--EQPMVNL 189
DB 147 SYHRSESEVAALNRYFGGLKSGGNAYVIGDPAKQKWHVYATYEP--EQPMVNL 205
QY 190 CMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFPFCGYSMAI 249
DB 206 CMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFPFCGYSMAI 261
QY 250 SAFSTHTVTPEDGFSYASVEMGLDATALSYGLVKRLRCFGPSEFSVAVTIFGGRGHA 309
DB 262 PAVSTHTVTPEDGFSYASVEMGLDATALSYGLVKRLRCFGPSEFSVAVTIFGGRGHA 314
QY 310 GTWKGKALGAEVYDCNNV-----EQELPGGLLVYQSF--CAEADAVATSPK 354
DB 315 DTADKVL--BOYCAVNVAGYCREGGVGLGVGGVLYQKGVATYVGLNKSPPK 367

RESULT 11
T12613
adenosylmethionine decarboxylase (EC 4.1.1.50) - common sunflower
N;Alternate names: S-adenosylmethionine decarboxylase
C;Species: Helianthus annuus (common sunflower)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12613
R;Eliasson, A.; Hammann, P.; Steinmetz, A.
submitted to the EMBL Data Library, May 1998
A;Description: Coding sequence for an S-adenosylmethionine decarboxylase from sunflower
A;Reference number: Z17552
A;Accession: T12613
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-361 <ELI>
A;Cross-references: UNIPROT:O65354; EMBL:AF066078; NID:g3153905; PID:g3153906

A;Experimental source: cultivar HA300; mature pollen
C;Genetics:
A;Gene: SAD
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;68/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 41.9%; Score 879; DB 2; Length 361;
Best Local Similarity 53.08; Pred. No. 9.2e-67;
Matches 199; Conservative 47; Mismatches 96; Indels 28; Gaps 11;

QY 13 SAIGFEGYKRLIEITPSEAPVFDPHGRGLRALSRQAIDSVDLRLARCTIVSELSNKKDFD 72
DB 3 SAIGFEGYKRLIEITPSEAPVFDPHGRGLRALSRQAIDSVDLRLARCTIVSELSNKKDFD 62
QY 73 SYLVSESLFIYPLKIVIKTCGTTKLLTTPRIELAEELSMPAAVYKSGRTFFPGAQ 132
DB 63 SYLVSESLFIYPLKIVIKTCGTTKLLTTPRIELAEELSMPAAVYKSGRTFFPGAQ 122
QY 133 APHRSESEVAALNRYFGGLKSGGNAYVIGDPAKQKWHVYATYEP-----PMVN 186
DB 123 FPHRSFTEEVVWLDLSDHFGKMGCSNAYVMGSAEKDQKWHVYASASANLVTQTAPVYT 181
QY 187 LEMCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFPFCGYSMA 246
DB 182 LEMCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFPFCGYSMA 237
QY 247 IHGSAFSTHTVTPEDGFSYASVEMGLDATALSYGLVKRLRCFGPSEFSVAVTIFGGR 306
DB 238 IEGDAISTHTVTPEDGFSYASVEMGLDATALSYGLVKRLRCFGPSEFSVAVTIFGGR 292
QY 307 GHAGTWKGKALGAEVYDCNNV-----NMVE---OELPG--GGLLVYQSFCAEADAVATSPKSVFH 358
DB 293 GNEVV--VKOLLENNDVNVKGVNVEETKFEVLGEGGSMVYGF--ARGGSCGSPRSTLH 350
QY 359 --CF--DGENVE 366
DB 351 RCWSETENEE 360

RESULT 12
T10750
probable adenosylmethionine decarboxylase (EC 4.1.1.50) - leaf mustard
C;Species: Brassica juncea (leaf mustard)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10750
R;Lee, T.; Liu, J.J.; Pua, E.C.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z17116
A;Accession: T10750
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-369 <LEE>
A;Cross-references: UNIPROT:O49972; EMBL:U80916; NID:g2662405; PID:g2662406
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;69/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 41.7%; Score 874.5; DB 2; Length 369;
Best Local Similarity 50.5%; Pred. No. 2.3e-66;
Matches 187; Conservative 51; Mismatches 89; Indels 43; Gaps 10;

QY 12 VSAIGFEGYKRLIEITPSEAPVFDPHGRGLRALSRQAIDSVDLRLARCTIVSELSNKKDFD 71
DB 3 VSAIGFEGYKRLIEITPSEAPVFDPHGRGLRALSRQAIDSVDLRLARCTIVSELSNKKDFD 62
QY 72 SYLVSESLFIYPLKIVIKTCGTTKLLTTPRIELAEELSMPAAVYKSGRTFFPGAQ 131
DB 63 SYLVSESLFIYPLKIVIKTCGTTKLLTTPRIELAEELSMPAAVYKSGRTFFPGAQ 122
QY 132 PAHRSESEVAALNRYFGGLKSGGNAYVIGDPAKQKWHVYATYEP-----EQP 183
DB 123 PPHRNFSESVLDGHHFAKMGSLSSVAYLMDGDDDT--KKWHV--YSASAPARNNGNNNN 180

Search completed: May 11, 2005, 22:59:08
Job time : 23.3058 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2005, 22:40:28 ; Search time 81.6495 Seconds
(without alignments)
1620.151 Million cell updates/sec

Title: US-10-732-923-406

Perfect score: 2118

Sequence: 1 MTVTIKELTNHNYIDHELSEA.....KIVYDLDDVHLFYMKLQKXI 396

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1432185 segs, 334051727 residues

Total number of hits satisfying chosen parameters: 1432185

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2118	100.0	396	15	US-10-310-154-456 Sequence 456, App
2	2118	100.0	396	15	US-10-369-493-22338 Sequence 22338, A
3	709.5	33.5	478	15	US-10-436-327-3 Sequence 3, Appli
4	681	32.2	503	15	US-10-369-493-3386 Sequence 3386, Ap
5	565	26.7	369	15	US-10-369-493-2553 Sequence 2553, Ap
6	471	22.2	348	9	US-09-925-300-1167 Sequence 1167, Ap
7	470	22.2	334	15	US-10-341-434-12 Sequence 12, Appl
8	470	22.2	334	15	US-10-341-434-20 Sequence 20, Appl
9	470	22.2	334	17	US-10-341-434-127 Sequence 127, App
10	470	22.2	334	17	US-10-753-267-50 Sequence 50, Appl
11	434	20.5	368	15	US-10-369-493-5286 Sequence 5286, Ap
12	434	20.5	368	15	US-10-369-493-5297 Sequence 5297, Ap
13	390	18.4	398	16	US-10-767-701-46359 Sequence 46359, A

Sequence 57997, A
Sequence 67343, A
Sequence 47033, A
Sequence 36776, A
Sequence 249854, A
Sequence 249859, A
Sequence 46255, A
Sequence 46648, A
Sequence 458, App
Sequence 46141, A
Sequence 249855, A
Sequence 43048, A
Sequence 46323, A
Sequence 47297, A
Sequence 147033, A
Sequence 147475, A
Sequence 4, Appli
Sequence 142921, A
Sequence 142922, A
Sequence 128930, A
Sequence 71868, A
Sequence 205003, A
Sequence 166485, A
Sequence 457, App
Sequence 205002, A
Sequence 56960, A
Sequence 39365, A
Sequence 69727, A
Sequence 45581, A
Sequence 159442, A
Sequence 56490, A
Sequence 57416, A

ALIGNMENTS

RESULT 1

US-10-310-154-456
; Sequence 456, Application US/10310154
; Publication No. US20030233670A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Chomet, Paul S.
; APPLICANT: Adams, Thomas H
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Agarwal, Ameeta K.
; APPLICANT: Ahrens, Jeffrey E.
; APPLICANT: Ball, James A.
; APPLICANT: Banu, G.
; APPLICANT: Bell, Erin
; APPLICANT: Boddupalli, Raghava
; APPLICANT: Deikman, Jill
; APPLICANT: Deng, Molian
; APPLICANT: Dong, Jinzhao
; APPLICANT: Duff, Stephen M.
; APPLICANT: Galligan, Meghan M.
; APPLICANT: Hinchey, Brenda S.
; APPLICANT: Huang, Shihshieh
; APPLICANT: Johnson, G. Richard
; APPLICANT: Jung, Vincent
; APPLICANT: Kretzmer, Keith A
; APPLICANT: Laccetti, Lucille B.
; APPLICANT: Lai, Chao-Qiang
; APPLICANT: Lee, Gary
; APPLICANT: Lin, Jie-Yi
; APPLICANT: Liu, Jingdong
; APPLICANT: Lu, Bin
; APPLICANT: Luethy, Michael M.
; APPLICANT: Lund, Adrian
; APPLICANT: Madson, Linda L.
; APPLICANT: Malloy, Kathleen A.
; APPLICANT: McKiel, Christine L.

```

; APPLICANT: Miller, Philip W.
; APPLICANT: Padmavathi, Manchikanti
; APPLICANT: Parnell, Laurence D.
; APPLICANT: Start, William G.
; APPLICANT: Tennesen, Dan
; APPLICANT: Vidya, K.R.
; APPLICANT: Wang, Haiyun
; APPLICANT: Xin, Zhanguo
; APPLICANT: Xu, Nanfei
; APPLICANT: Yang, Chunzhi
; APPLICANT: Zeng, Xiaoping
; APPLICANT: Zhang, Qiang
; APPLICANT: Zhao, Yajuan
; APPLICANT: Zhou, Li
; TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
; FILE REFERENCE: 38-15(52796)B
; CURRENT APPLICATION NUMBER: US/10/310,154
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,358
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 736
; SEQ ID NO 456
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-310-154-456

Query Match      100.0%; Score 2118; DB 15; Length 396;
Best Local Similarity 100.0%; Pred. No. 3.9e-186;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTVTIKELTNHNYIDHLSATLSDTAFAEGPEKLEIWFPPHKKSIITTEKTLRNIGMDRW 60
Db 1 MTVTIKELTNHNYIDHLSATLSDTAFAEGPEKLEIWFPPHKKSIITTEKTLRNIGMDRW 60
Qy 61 IEILKLVKCEVLSMKYTKELDAPLLSSSLFVFDHKLTMKTCGTTTTLFCLEKLFQIVEQ 120
Db 61 IEILKLVKCEVLSMKYTKELDAPLLSSSLFVFDHKLTMKTCGTTTTLFCLEKLFQIVEQ 120
Qy 121 ELSWAFRTTGGKYKPKFVYSRRCFLFPCQAAIHQNWADVDVYLNKFFDNGKSYSGVR 180
Db 121 ELSWAFRTTGGKYKPKFVYSRRCFLFPCQAAIHQNWADVDVYLNKFFDNGKSYSGVR 180
Qy 181 NDKSNHNLVYVETDRSTPGKEYIEDDDTFFVLMTELDPCEASKFVCGPEASTTALVE 240
Db 181 NDKSNHNLVYVETDRSTPGKEYIEDDDTFFVLMTELDPCEASKFVCGPEASTTALVE 240
Qy 241 PNEDKGHNLGQYQMTKNTLRLDEIYVNSAQSDLSLPHHDAFAFTPCGYSSNMLAEKYIYTL 300
Db 241 PNEDKGHNLGQYQMTKNTLRLDEIYVNSAQSDLSLPHHDAFAFTPCGYSSNMLAEKYIYTL 300
Qy 301 HVTPEKGSVASFESNIPVFDISQKQDNLDVLLHILNVFPQREFSMTFTTKYQNSQSFQ 360
Db 301 HVTPEKGSVASFESNIPVFDISQKQDNLDVLLHILNVFPQREFSMTFTTKYQNSQSFQ 360
Qy 361 KLLSINESLPDYIKLKIYVDLDYHLYFMKLOKKI 396
Db 361 KLLSINESLPDYIKLKIYVDLDYHLYFMKLOKKI 396

RESULT 2
US-10-369-493-22338
; Sequence 22338, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B

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; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 22338
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-22338

Query Match      100.0%; Score 2118; DB 15; Length 396;
Best Local Similarity 100.0%; Pred. No. 3.9e-186;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTVTIKELTNHNYIDHLSATLSDTAFAEGPEKLEIWFPPHKKSIITTEKTLRNIGMDRW 60
Db 1 MTVTIKELTNHNYIDHLSATLSDTAFAEGPEKLEIWFPPHKKSIITTEKTLRNIGMDRW 60
Qy 61 IEILKLVKCEVLSMKYTKELDAPLLSSSLFVFDHKLTMKTCGTTTTLFCLEKLFQIVEQ 120
Db 61 IEILKLVKCEVLSMKYTKELDAPLLSSSLFVFDHKLTMKTCGTTTTLFCLEKLFQIVEQ 120
Qy 121 ELSWAFRTTGGKYKPKFVYSRRCFLFPCQAAIHQNWADVDVYLNKFFDNGKSYSGVR 180
Db 121 ELSWAFRTTGGKYKPKFVYSRRCFLFPCQAAIHQNWADVDVYLNKFFDNGKSYSGVR 180
Qy 181 NDKSNHNLVYVETDRSTPGKEYIEDDDTFFVLMTELDPCEASKFVCGPEASTTALVE 240
Db 181 NDKSNHNLVYVETDRSTPGKEYIEDDDTFFVLMTELDPCEASKFVCGPEASTTALVE 240
Qy 241 PNEDKGHNLGQYQMTKNTLRLDEIYVNSAQSDLSLPHHDAFAFTPCGYSSNMLAEKYIYTL 300
Db 241 PNEDKGHNLGQYQMTKNTLRLDEIYVNSAQSDLSLPHHDAFAFTPCGYSSNMLAEKYIYTL 300
Qy 301 HVTPEKGSVASFESNIPVFDISQKQDNLDVLLHILNVFPQREFSMTFTTKYQNSQSFQ 360
Db 301 HVTPEKGSVASFESNIPVFDISQKQDNLDVLLHILNVFPQREFSMTFTTKYQNSQSFQ 360
Qy 361 KLLSINESLPDYIKLKIYVDLDYHLYFMKLOKKI 396
Db 361 KLLSINESLPDYIKLKIYVDLDYHLYFMKLOKKI 396

RESULT 3
US-10-436-327-3
; Sequence 3, Application US/10436327
; Publication No. US20030224970A1
; GENERAL INFORMATION:
; APPLICANT: Mahanty, Sanjoy K
; APPLICANT: Heiniger, Ryan W
; APPLICANT: Skalchunes, Amy R
; APPLICANT: Pan, Huaqin
; APPLICANT: Tarpey, Rex
; APPLICANT: Shuster, Jeffrey R
; APPLICANT: Tanzer, Matthew M
; APPLICANT: Hamer, Liebeth
; APPLICANT: Adachi, Kilchi
; APPLICANT: DeZwaan, Todd M
; APPLICANT: Lo, Sze Chung C
; APPLICANT: Montenegro-Chamorro, Maria V
; APPLICANT: Frank, Sheryl A
; APPLICANT: Darveaux, Blaise A
; TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF INHIBITORS OF
; TITLE OF INVENTION: S-ADENOSYLMETHIONINE DECARBOXYLASE AS ANTIBIOTICS
; FILE REFERENCE: 2151US
; CURRENT APPLICATION NUMBER: US/10/436,327
; CURRENT FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 3
; LENGTH: 478
; TYPE: PRT

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ORGANISM: Magnaporthe grisea
US-10-436-327-3

Query Match 33.5%; Score 709.5; DB 15; Length 478;
Best Local Similarity 35.2%; Pred. No. 2.3e-56;
Matches 162; Conservative 86; Mismatches 115; Indels 97; Gaps 15;

QY 14 IDHLSATLDSTDAFEGPEKLLBIWFFPHKSI---TTEKTLRNIGMDRWIEILKLVKCE 70
DB 23 INHDVAQDLDSGAFAFEGPEKLLBIWFFPHKSI---TTEKTLRNIGMDRWIEILKLVKCE 82

QY 71 VLSMKTKELDALFLSSSLFVFDHKLTKMTCTGTTTTLFCLEKLFQI----- 117
DB 83 ILSVQSSVVDAYLLSSSMFVFPKILTKCTGTTTTLGLAQLRLAAVADAGFPVHNAS 142

QY 118 -VQELSWAPRTTGGKPKFYRRRCFLFPCKQAAIHONNADEVDYLNKFFDNGKSY 176
DB 143 SVDEKAAA-----TPRYFYSRKNFLFPDRQGRPHRSKWQVKYLDSPFEGGSAY 193

QY 177 SVGRNDSNHNLYVTE-----TDRSTPKGKEYI-----EDDDTEFVLMTL 219
DB 194 MVGKMN-GDHWLYMTSPGSTALTTPQTPPAGELMRIPTGLQTAASREDDTEFLVMTDL 252

QY 220 DPCASKFVCGPASTTA-----LVEPNEDKGNLGY 251
DB 253 DPNKQFYL-EQASALACKQATLAQQAEEAHAALDKAASTDEQLVSEALATTEGHALGT 311

QY 252 QMTKNTLRDIYVNSA-QSDLSFHHDAFAFTPCGYSSNMIL-----AEKYYVT 299
DB 312 VSDTCLSDVYPKSKYDPDARI---DAYMFEPCGSANGVVPAPPDATGAQGGNEHYFT 367

QY 300 LHYTPKGSYASFPESNIPVFDISQKQDNLVLLHLNVPQPREFSMTFT-KNYQNOS 358
DB 368 VHYTPENCYSASFETNVPG---GQNGRETADIIGHVVGIFKPGFSTVTLFEGKGRGEN 424

QY 359 FQKL---LSINESLPDIKDKIVYLDLDDVHLFYMKLQKK 395
DB 425 GTRADQRLRV-DNVPGYRLQDKIVHEDDYDLVFRFYQRE 463

RESULT 4
US-10-369-493-3386
; Sequence 3386, Application US/10369493;
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 3386
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Neurospora crassa
US-10-369-493-3386

Query Match 32.2%; Score 681; DB 15; Length 503;
Best Local Similarity 32.5%; Pred. No. 1.1e-53;
Matches 161; Conservative 85; Mismatches 128; Indels 122; Gaps 13;

QY 2 TVTIKELTNNYIDHLSATLDSTDAFEGPEKLLBIWFFPHKSI---TTEKTLRNIGMD 58
DB 14 TFSPEGTPTLTINHVAADLSDTNAFEGPEKLLBIWFFPHKSI---TTEKTLRNIGMD 73

QY 59 RWIEILKLVKCEVLSMKTKELDALFLSSSLFVFDHKLTKMTCTGTTTTLFCLEKLFQIV 118

DB 74 SWTPMLDLVHCKVLSIINSENVDSYLLSSSMFVFPKILTKCTGTTTTLGLDLMLRIA 133

QY 119 EQELSWAPRTTGGK---YKPFKYFYSRRRCFLFPCKQAAIHONNADEVDYLNKFFDNG 173

DB 134 AVDAGFPFHNVASLEDPKVAATPLRVFYSRKNFLFPQKQGRPHRSKWQVKYLDSPFEGGSAY 193

QY 174 KSYSGRNDKSNHNLYVTE-----TDRSTPKGKEYI-----TPKGEKYEID 207

DB 194 SAYMVGKMN-GDHWLYMTSPGSTALTTPQTPPAGELMRIPTGLQTAASREDDTEFLVMTDL 252

QY 208 DDTFPEVLMTLDPKASKFV-----CG----- 230

DB 253 ADTEILMTDLDPENAKKFLYEEATAIAKEKLFKSEANGDASFDVSSSGDCDADGQA 312

QY 231 --PEASTTALVERNEDEKGNLGYQMTKNTLRDIYVNSA-QSDLSFHHDAFAFTPCGYS 287

DB 313 ILPEALT-----EGHALGTVVSEACGLSVYPTSTYDPDARI---DAYQFSPCGFS 360

QY 288 SNMIL-----AEKYYVTTHVTPEKGSYASFPESNIPVFDISQKQDNLVLLHI 336

DB 361 ANGVPVAVAGADGTIPKSGHYFTVHTVPEQCSFASFETNVPG---GQNGRQTAETVIEQV 417

QY 337 LNVQPREFSMTFT-----TKYQNSQSFQKLLSINESLPDIKDKIV 379

DB 418 VNIIFRGRFSTVTLFEAKGALATTPGEDADDSRRSWSGAAAKQRMERIN---GYRRVDRIV 473

QY 380 YLDLDDVHLFYMKLQKK 395

DB 474 HDEFYDLVFRYYERE 489

RESULT 5
US-10-369-493-2553
; Sequence 2553, Application US/10369493;
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2553
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-10-369-493-2553

Query Match 26.7%; Score 565; DB 15; Length 369;
Best Local Similarity 36.1%; Pred. No. 3.2e-43;
Matches 139; Conservative 75; Mismatches 135; Indels 36; Gaps 13;

QY 14 IDHLSATLDSTDAFEGPEKLLBIWFFPHKSI---TTEKTLRNIGMDRWIEILKLVK 68
DB 7 VQDENSEEP-NTSSFEGPEKLLBIWFFPHKSI---TTEKTLRNIGMDRWIEILKLVK 65

QY 69 CEVLSMKTKELDALFLSSSLFVFDHKLTKMTCTGTTTTLFCLEKLFQIVQELSWAPRT 128

DB 66 CKVLSVNSEEDAYLLSSSMFVFPKILTKCTGTTTTLGLAQLRLAAVADAGFPVHNAS 115

QY 129 TGGKPKFYRRRCFLFPCKQAAIHONNADEVDYLNKFFDNGKSYSGRNDKSNHN 188

DB 116 SSVGFDRPRLIRFYSRKNFLYPERQLAPHTSWESEVYQLQFPFSGGCVVGPNTK-NHWH 174

QY 189 LYVTETDRSTPKGKEYIEDDDTEFVLMTLDPKASKF-----VCGPEASTTALVEP 241

Db 175 LFSLDADYSL-EDSLDPEDETLEVLMTDMSPEISQFYAPSLDVRSGDDYVREKN 233
Qy 242 NEDKGNLGYQMTKNTRLDIYVNSAQDLSLFFHDAFAFTPCGYSSNMILAKEYVYTLH 301
Db 234 NLSGGHILGSVADESGVRLCSTSDKAVL---DAFQEPFIFGSSNMIYKDR-YATIH 288
Qy 302 VTPKKGHSYASFENIPVFDISQKQNDLVLLHILNVFQPREFMTFTTKYQNSFOK 361
Db 289 VTPQHCYSYASFETNVSQFQGRSISETIE---KTVKTFGANKFCLTLFOAKGASQ--EK 343
Qy 362 LLSIN-ESLPDYIKLXIVVDLDY 385
Db 344 HFSKLSKFSYKREFFIVDFPGY 368

RESULT 6

US-09-925-300-1167
; Sequence 1167, Application US/099255300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P4101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 1167
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-300-1167

Query Match 22.2%, Score 471; DB 9; Length 348;

Best Local Similarity 30.3%; Pred. No. 1.3e-34;

Matches 115; Conservative 70; Mismatches 138; Indels 56; Gaps 10;

Qy 22 LDSTDAFEGPEKLEIWFPHHKSIT- EKTLRNIGMDRWIEILKLVKCEVLSMKTTEL 80
Db 15 MEAAHFFEGTEKLELVNFSRQPDANQSGDLRTIPRSEWDILKDVQCSIIISVTKDKQ 74
Qy 81 DAPLLSESSLFVFDHKLTMKTCGTTTLFCLEKLFQIVEQELSFAFRTTQGGKYKPF--- 137
Db 75 EAYVLSSESMFVSKRRFILKTCGTITLLKALVPLLLKARD-----YSGFDSI 121
Qy 138 -KVFSRRCLFPCKQAAIHONWADEVYLNKFDNGKYSVGRNDKSNHNLVYVTTDR 196
Db 122 QSPFYSRKNFMKPSHQGYPHRFQEEIEFLNAIFPNGAAYCMGRMN-SDCWLYLTLDPE 180
Qy 197 STPKGEYIEDDDTFFVLMTELDPEKASFCVCPPEASTTALVEPNEDKGNLGYQTKN 256
Db 181 S-----RVISQPDQTLSEILMSELDPAVMDOFYM-----KOGVTAKOVRE 220
Qy 257 TRLDIYVNSAQDLSLFFHDAFAFTPCGYSSNMILAKEYVYTLHVTPEKGSYASPE 316
Db 221 SGIRDLPGSVIATM-----FNPCGYSMGKMSDGYWIHTIPEPEFSVSVETN 272
Qy 317 IPVFDISQKQNDLVLLHILNVFQPREFMTFTTKYQNSFOKLSINESLPDYIKLD 376
Db 273 -----LSQTSYD--DLIRKVEVEFKPGKFTVTLFVN--QSSKCRVTLASPKIEGPKRLD 323
Qy 377 KIVYDLDYHLFYMKLOKK 395
Db 324 CQSAFNDYNFVFTSFAKK 342

RESULT 7

US-10-341-434-12
; Sequence 12, Application US/10341434
; Publication No. US20030215835A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
; FILE REFERENCE: 9U 204 205 R1
; CURRENT APPLICATION NUMBER: US/10/341,434
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/348,164
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/348,119
; PRIOR FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 12
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-341-434-12

Query Match 22.2%, Score 470; DB 15; Length 334;

Best Local Similarity 30.3%; Pred. No. 1.5e-34;

Matches 115; Conservative 69; Mismatches 139; Indels 56; Gaps 10;

Qy 22 LDSTDAFEGPEKLEIWFPHHKSIT- EKTLRNIGMDRWIEILKLVKCEVLSMKTTEL 80
Db 1 MEAAHFFEGTEKLELVNFSRQPDANQSGDLRTIPRSEWDILKDVQCSIIISVTKDKQ 60
Qy 81 DAPLLSESSLFVFDHKLTMKTCGTTTLFCLEKLFQIVEQELSFAFRTTQGGKYKPF--- 137
Db 61 EAYVLSSESMFVSKRRFILKTCGTITLLKALVPLLLKARD-----YSGFDSI 107
Qy 138 -KVFSRRCLFPCKQAAIHONWADEVYLNKFDNGKYSVGRNDKSNHNLVYVTTDR 196
Db 108 QSPFYSRKNFMKPSHQGYPHRFQEEIEFLNAIFPNGAGYCMGRMN-SDCWLYLTLDPE 166
Qy 197 STPKGEYIEDDDTFFVLMTELDPEKASFCVCPPEASTTALVEPNEDKGNLGYQTKN 256
Db 167 S-----RVISQPDQTLSEILMSELDPAVMDOFYM-----KOGVTAKOVRE 206
Qy 257 TRLDIYVNSAQDLSLFFHDAFAFTPCGYSSNMILAKEYVYTLHVTPEKGSYASPE 316
Db 207 SGIRDLPGSVIATM-----FNPCGYSMGKMSDGYWIHTIPEPEFSVSVETN 258
Qy 317 IPVFDISQKQNDLVLLHILNVFQPREFMTFTTKYQNSFOKLSINESLPDYIKLD 376
Db 259 -----LSQTSYD--DLIRKVEVEFKPGKFTVTLFVN--QSSKCRVTLASPKIEGPKRLD 309
Qy 377 KIVYDLDYHLFYMKLOKK 395
Db 310 CQSAFNDYNFVFTSFAKK 328

RESULT 8

US-10-341-434-20
; Sequence 20, Application US/10341434
; Publication No. US20030215835A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
; FILE REFERENCE: 9U 204 205 R1
; CURRENT APPLICATION NUMBER: US/10/341,434
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/348,164
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/348,119
; PRIOR FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 20
; LENGTH: 334
; TYPE: PRT


```

; ORGANISM: Homo sapiens
US-10-341-434-20

Query Match      22.2%; Score 470; DB 15; Length 334;
Best Local Similarity 30.3%; Pred. No. 1.5e-34;
Matches 115; Conservative 69; Mismatches 139; Indels 56; Gaps 10;

QY 22 LDSTDAFEGPEKLEIWPFPKHSITT-EKTLRNIGMDRWIEILKVKCEVLSMKTKEL 80
DB 1 MEAAHFFEGTEKLEWFSRQDPDANQSGDLRTIPRSEWDILLKDVQCSIIVTKTDKQ 60
QY 81 DAFLISESSLFVFDHKLTKMKTCTTTTLFCLEKLFQIVEQELSWAFRTTQGGKYKPF--- 137
DB 61 EAVLSESSMFYSKRRFILTCTGTTLLKALVPLKLARD-----YSGFDSI 107
QY 138 -KVFSRRRCFLPCKQAAIHQWDAVEDVYLNKFPDNGKSYSGVRNDKSNHNLVYTTEDR 196
DB 108 QSFFYSRKNFMKPSHQYFHRNFQEBIEFLNALFPNGAGYCWGRWN-SDCWLYLTLDFFE 166
QY 197 STPKGKEYIEDDETFEVLMTLDEPCASKFVCGPEASTTALVPEPNEDKGNHLGYQMTKN 256
DB 167 S-----RVISQDPQDTLEILMSLSDPAVMDQFYM-----KCGVTAKDVTR 206
QY 257 TRLDEIYVNSAODSLSFHHDAFAFTPCGYSNNMILAEEKYYTTLHVTPEKGSVSPESN 316
DB 207 SGIRDLIPGSVIDATM-----FNPCCYSGMNGKMSDGTWYTHITPEPFSYVSFETN 258
QY 317 IPVFIDISQCKQDNLDVLLHILNVFQPRFBSMTFFTKYQNSQFQKLLSINESLDPYIKLD 376
DB 259 -----LSQTSYD--DLIRKVEVFPGKGVITLFLVN--QSSKCRVTLASPKIEGFKRLD 309
QY 377 KIYDLDVYHLYFMKLQKK 395
DB 310 CQSAMFNDYNFVFTSFPAKK 328

RESULT 9
US-10-341-434-127
; Sequence 127, Application US/10341434
; Publication No. US20030215835A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
; FILE REFERENCE: 9U 204 205 R1
; CURRENT APPLICATION NUMBER: US/10/341,434
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/348,164
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/348,119
; PRIOR FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 127
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-341-434-127

Query Match      22.2%; Score 470; DB 15; Length 334;
Best Local Similarity 30.3%; Pred. No. 1.5e-34;
Matches 115; Conservative 69; Mismatches 139; Indels 56; Gaps 10;

QY 22 LDSTDAFEGPEKLEIWPFPKHSITT-EKTLRNIGMDRWIEILKVKCEVLSMKTKEL 80
DB 1 MEAAHFFEGTEKLEWFSRQDPDANQSGDLRTIPRSEWDILLKDVQCSIIVTKTDKQ 60
QY 81 DAFLISESSLFVFDHKLTKMKTCTTTTLFCLEKLFQIVEQELSWAFRTTQGGKYKPF--- 137
DB 61 EAVLSESSMFYSKRRFILTCTGTTLLKALVPLKLARD-----YSGFDSI 107
QY 138 -KVFSRRRCFLPCKQAAIHQWDAVEDVYLNKFPDNGKSYSGVRNDKSNHNLVYTTEDR 196
DB 108 QSFFYSRKNFMKPSHQYFHRNFQEBIEFLNALFPNGAGYCWGRWN-SDCWLYLTLDFFE 166
QY 197 STPKGKEYIEDDETFEVLMTLDEPCASKFVCGPEASTTALVPEPNEDKGNHLGYQMTKN 256
DB 167 S-----RVISQDPQDTLEILMSLSDPAVMDQFYM-----KCGVTAKDVTR 206
QY 257 TRLDEIYVNSAODSLSFHHDAFAFTPCGYSNNMILAEEKYYTTLHVTPEKGSVSPESN 316
DB 207 SGIRDLIPGSVIDATM-----FNPCCYSGMNGKMSDGTWYTHITPEPFSYVSFETN 258
QY 317 IPVFIDISQCKQDNLDVLLHILNVFQPRFBSMTFFTKYQNSQFQKLLSINESLDPYIKLD 376
DB 259 -----LSQTSYD--DLIRKVEVFPGKGVITLFLVN--QSSKCRVTLASPKIEGFKRLD 309
QY 377 KIYDLDVYHLYFMKLQKK 395
DB 310 CQSAMFNDYNFVFTSFPAKK 328

RESULT 9
US-10-753-267-50
; Sequence 50, Application US/10753267
; Publication No. US20050037946A1
; GENERAL INFORMATION:
; APPLICANT: Millenium Pharmaceuticals, Inc.
; APPLICANT: Stagliano, Nancy E.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Donoghue, Mary A.
; APPLICANT: Rodrigue-Way, Amelie
; APPLICANT: Tomlinson, James E.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553
; TITLE OF INVENTION: 10653, 9235, 21668, 17794, 2210, 6169, 10102, 21061, 1
; TITLE OF INVENTION: 1468, 12282, 6350, 9035, 1820, 23652, 7301, 8925, 8701
; TITLE OF INVENTION: 3533, 94622, 9123, 12788, 17729, 65552, 1261, 21476, 333
; TITLE OF INVENTION: 9380, 2569854, 33556, 53656, 44143, 32612, 10671, 261
; TITLE OF INVENTION: 44570, 41922, 2552, 2417, 19319, 43969, 8921, 8993, 955
; TITLE OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408
; TITLE OF INVENTION: 42028, 112091, 13886, 13942, 1673, 54946 OR 2419
; FILE REFERENCE: MPI03-003P1RNMNM
; CURRENT APPLICATION NUMBER: US/10/753,267
; CURRENT FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: US 60/439,683
; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/445,216
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,036
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/454,189
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/457,541
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 60/466,411
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 60/469,041
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/477,414
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US 60/478,560
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/489,772
; PRIOR FILING DATE: 2003-07-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-753-267-50

Query Match      22.2%; Score 470; DB 17; Length 334;

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Best Local Similarity 30.3%; Pred. No. 1.5e-34;
Matches 115; Conservative 69; Mismatches 139; Indels 56; Gaps 10

QY 22 LDSTDAFEGPEKLEIWFPHKKSIIT--EKTLRNIGMDRWIEILKLVKEVLSMKTKTEL 80
Db 1 MEAAHFEGTEKLELVFWSRQOPDANQSGGDLRTIPRSEWDILLKDVQCSIISVTKTDKQ 60

QY 81 DAFLLSSSLFVFDHKLMTKTCGTTTTLFLCLLEKLFQIVEQELSWAFFRTQGGKYKPF--- 137
Db 61 EAYVLSSSMFVSKRRFILTKTCGTTTLLKALVPLLLKLRD-----YSGFDSI 107

QY 138 -KVPSRRCLFPCQAAIHQWADAEDVDYLKNKFPDNGSKSVGRNDKSNHNLYYTETDR 196
Db 108 QSFYSRKNFMKPSHQGYPHRFNFOEBIEFLNAIPNGAGYCWGRMN-SDCVLYLTLDPE 166

QY 197 STPKGEYIEDDDSTFEVLMTDELPOCECAKSKVCGPEASTTALVEPNEDKGNLGYQMTKN 256
Db 167 S-----RVISQPDQTLSELMSELDPAVMDQYM-----KOGVTAKDVTRE 206

QY 257 TRLDEIVNQAQSDSLSPHDAFAFTPCGYSSNMILAEKYYTTLHVTPEKGSVASFESN 316
Db 207 SGIRDLLPGSVIDATM-----FNP CGYSWMGMSDGTWTHTITEPEFSYVSFTN 258

QY 317 IPVEDISQGDNDLVLLHILNVQPRFESMTFTKNYQNSQFQKLLSINSLPDYIKLD 376
Db 259 -----LSQTSYD--DLIRKVVVEFKPGKFTVTLFVN--QSSKRTVLASPKIEGFKELD 309

QY 377 KIVYDLDYHLFYMKLQKK 395
Db 310 QCSAMFNDYNFVFTSFAKK 328

RESULT 11
US-10-369-493-5296
; Sequence 5296, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5296
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5296

Query Match 20.5%; Score 434; DB 15; Length 368;
Best Local Similarity 30.9%; Pred. No. 3.7e-31;
Matches 125; Conservative 72; Mismatches 129; Indels 78; Gaps 16

QY 9 TNNHYIDHEISATLSDTDAFEGPEKLEIWFPHKKSIITTEKTLRNIGMDRWIEILKLVK 68
Db 7 TNFAVQTHPVKAP-DEEYVFEGAEKLELWFCSSQTNET--RSRLIIPREEDAMLDIAR 63

QY 69 CEVLSMKTKTELDAFLSSESLFVPFDHKLTMKTCGTTTTLFCLEKLFQIVBQELSWAFRT 128
Db 64 CKILSKHNEISIDSVLSSESLFISDNRVILKTCGTTTLLAALPVIMQ-----LAGAY-- 116

QY 129 TQGGKYKPFKYVSRRCFLPCKQAAIHQWADAEDVDYLKNKFPDNGSKSVGRNDKSNHN 188
Db 117 --AGLDQVQSYYYSRKNFLPDLPQSLHKNFDAEVEYLDLSFFVDGHAYCLG-SLKQDRWY 173

QY 189 LYVTETDRSTPKGXEYIEDDDSTFEVLMTDELPOCECAKSKVCGPEASTTALVEPNEDKGN 248

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; OTHER INFORMATION: Clone ID: UC-ZMFLMO17023A12_FLI.pcp
US-10-425-114-57957

Query Match      18.3%; Score 388; DB 15; Length 416;
Best Local Similarity 33.1%; Pred. No. 7.5e-27;
Matches 111; Conservative 56; Mismatches 110; Indels 58; Gaps 14;

Qy 24 STDAFGPEKLRIEWFPHPKKSITTE---KTLBNIGMDRWIEILKLVKCEVLSMKKTKE 80
Db 36 SVTGFGEFKRLRISF--SEAPVLADPSGRLGLRALRAQDVSVDLARCITVSELSNDDF 93

Qy 81 DAFLLSESSLFVFDHKLTMKTCGTTTTFLCLEKLFQIVEQELSWAFFTTGGKYKPF-KV 139
Db 94 DSYVLSSESLFVYPYKIVIKTCTTKLLLLAI PRILELABELL-----LPLAAV 141

Qy 140 FYSRRCFLFPCKQAAATHONWADEVLYLNKPF----DNGKSYSYGRNDK-SNHWNLYVTET 194
Db 142 KYSRGTFIFPEAQPSPHKNFADEVFLNRFPGGLKGGNAYVIGDSAKPQGRWHVYV--- 198

Qy 195 DRSTPGKGEYIDDDDETFFVIMTLELDPCEASKFVCGPEASTTALVEPNEDKGHNL-GYQM 253

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Qy	254	TKNTRLDEIYVNSAQSDSDFHRHDAFPTCGSYSSNMILAEKYTYTLHTVTPEKGWSYASF	313
	:	:	:
Dd	241	TKLSGISDI-IPMEICD-----FDPEFCGYSMNAVHGPA-LSTIHVTPEDGSFYASY	291
	:	:	:
Qy	314	ESNIPVPDISQGDNDLVDLLHLINLVFPQPREFSMT	348
	:	:	:
Dd	292	E----VMGFNPGSFGDLVKRVLCRFGPTEFSVT	322
	:	:	:

RESULT 15
US-10-425-114--67343
; Sequence 67343, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated wi
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; PUBLICATION DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128

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;
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4767-001-F3_FLI.psp
US-10-425-114-67343

Query Match          18.1%; Score 388; DB 15; Length 416;
Best Local Similarity 33.1%; Pred. No. 7.5e-27;
Matches 111; Conservative 56; Mismatches 110; Indels 58; Gaps 14;

Qy 24  STDAFGPEKLLRIWFFPHKKSITTE---KTLRNIGHMDRWIEILKLVKCVLSMKTTEL 80
      ||||| ||||| : : : : : || : : : : :
Db 36  SVIGFEGFEKRLRISF--SEAPVLADPSGRGLRALGRAQIDSVLDLARCTIVSELSNDDF 93
      ||||| ||||| : : : : : || : : : : :

Qy 81  DAPLSSSIFVFDHLTKWTKCTGTTTLFLEKLFQIVQEQLSWAFRTTGGKYKPF-KV 139
      ||||| ||||| : : : : : || : : : : :
Db 94  DSVLSSSLFVVPYKIVIKTCTTKLLAIPRIELAEELL-----LPLAAV 141
      ||||| ||||| : : : : : || : : : : :

Qy 140 FYRRRCFLFPCKQAIIHQWNADEVYINKPF-----DNKGKSYSGRNDK-SNHWNLYVTET 194
      ||||| ||||| : : : : : || : : : : :
Db 142 KYRSGTFIPPEAQSPHKNFADEVAFILNFRFFGLKSGGNAYVIGDSAKPQKWHVYV--- 198
      ||||| ||||| : : : : : || : : : : :

```

```
QY 195 DRSTPKGKEYIEDDETEFEVLMTLDEPCASKFVCGPEASTTALVEBNEDEKGNL-GYOM 253
Db 199 -----AAEHPEEPVVTLEMCMTGLDKKASVFF-----KTTA-----DGYSLCAKEM 240
QY 254 TKNTRLDEIYVNSAQSDLSFHHDFAFTPCGYSSNMILAKEYYYTLHVTPKGSYASF 313
Db 241 TKLSGISDI-IPMEICD-----PDFEPCGYSMNAVHGPA-LSTIHVTPEDGFSYASY 291
QY 314 ESNIPVFDISQKQDNLDVLLHILNVFPQPREFSMT 348
Db 292 E-----VMGFNPGSFSYGDLVKRVLRCFGPTEFSVT 322
```

Search completed: May 11, 2005, 22:57:56
Job time : 83.6495 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 11, 2005, 22:39:42 ; Search time 26.1959 Seconds
(without alignments)
1128.461 Million cell updates/sec

Title: US-10-732-923-406
Perfect score: 2118
Sequence: 1 MTVTIKELTNHNYIDHELSEA.....KIVYDLDYHLYFMKLQKKI 396

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	785	37.1	424	4	US-09-248-796A-18169
2	471	22.2	348	4	US-09-949-016-10038
3	470	22.2	334	4	US-09-917-254-54
4	112	5.3	753	4	US-09-248-796A-19291
5	108.5	5.1	585	4	US-09-107-532A-5494
6	107.5	5.1	749	4	US-09-562-737-95
7	107	5.1	336	1	US-07-667-276A-8
8	99	4.7	1661	2	US-08-882-083-2
9	99	4.7	1661	3	US-08-558-107-2
10	99	4.7	1661	3	US-09-243-539-2
11	99	4.7	2184	4	US-09-417-485D-6
12	96.5	4.6	627	4	US-08-851-567B-28
13	96.5	4.6	822	4	US-09-248-796A-19917
14	96.5	4.6	1189	4	US-08-851-567B-26
15	95	4.5	944	2	US-08-867-941-23
16	95	4.5	944	3	US-09-074-658-23
17	94.5	4.5	554	3	US-09-319-989-6
18	94.5	4.5	2777	4	US-09-543-681A-6124
19	94	4.4	485	2	US-08-724-394A-8
20	94	4.4	695	3	US-09-134-001C-4341
21	94	4.4	754	4	US-09-710-279-1296
22	93.5	4.4	1183	2	US-08-447-031A-2
23	93	4.4	3418	3	US-08-755-587-44
24	92.5	4.4	2325	4	US-08-697-826A-10
25	92.5	4.4	2938	5	PCT-US94-00198-3
26	92	4.3	414	4	US-09-107-433-3170
27	92	4.3	423	4	US-09-583-110-3518

28	92	4.3	484	6	5171673-8	Patent No. 5171673
29	92	4.3	484	6	5171673-8	Patent No. 5171673
30	92	4.3	487	6	5171673-6	Patent No. 5171673
31	92	4.3	487	6	5171673-6	Patent No. 5171673
32	92	4.3	610	4	US-09-248-796A-17036	Sequence 17036, A
33	92	4.3	749	2	US-08-568-459A-6	Sequence 6, Appli
34	92	4.3	749	2	US-08-487-826B-6	Sequence 6, Appli
35	92	4.3	749	3	US-09-210-288-6	Sequence 6, Appli
36	92	4.3	2304	3	US-09-324-867-4	Sequence 8, Appli
37	92	4.3	2319	1	US-08-212-133A-8	Sequence 6, Appli
38	92	4.3	2319	1	US-08-474-503-6	Sequence 6, Appli
39	92	4.3	2319	2	US-08-670-707A-6	Sequence 6, Appli
40	92	4.3	2319	3	US-09-037-601-6	Sequence 6, Appli
41	92	4.3	2319	3	US-09-315-179-6	Sequence 6, Appli
42	92	4.3	2319	4	US-09-523-656-28	Sequence 28, Appli
43	92	4.3	2319	5	PCT-US94-13200-6	Sequence 6, Appli
44	91	4.3	686	4	US-09-107-532A-5118	Sequence 5118, Ap
45	90.5	4.3	592	3	US-08-845-258-24	Sequence 24, Appli

ALIGNMENTS

RESULT 1

US-09-248-796A-18169
; Sequence 18169, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18169
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18169

Query Match	37.1%	Score 785;	DB 4;	Length 424;
Best Local Similarity	43.8%	Pred. No. 1e-71;		
Matches	176;	Conservative 64;	Mismatches 114;	Indels 50; Gaps 12;
QY	13	YIDHLSATLDSFDAEGPEKLEIWFPPHKKSIITTEKTLRNICMDRWIELKLVKCEVL	72	
DB	50	YSNHELSTALDSTHAEQPEKLEIWFYSEKE--LSPINLRDIKFTDWIELNLVHCEVL	107	
QY	73	SMKKTKELDAFLSSESLFVDFHKLFMKTCGTTTTLFCLEKLFQIVEQEL--SWAFRTTQ	130	
DB	108	SKVSSNLDAFLSSESLFVFPFKIILKTCGTTTTLACLALLFETVKNELLQNEGLKATP	167	
QY	131	GGKYKPKFYFYSRCFLPCKQAAIHQNWADVDYLNKFPDNGKYSVGNKDKSNHNLV	190	
DB	168	QSK-NIYQIFYFYSRRSPFPDRQIHVHGNQEEVKLLNQYFNNKSYIVGN--TNHLY	223	
QY	191	V-----TETDRSTPKGKEYIEDDETFEVLMTDELDPCEASKFVCGPEASTAL	238	
DB	224	VGGNGTKPKPVASTTTTTTTP-----VVNDCTLEIMTQLSLEASQOFTTRKPGDTA	276	
QY	239	VEPNEDKGNHNGVQMTKNTRDLDEIYVNSAQ-----DSDLSPHDAFAFTPCGYSSNMI	291	
DB	277	IDSNDHLDLGGQELKQTLGNLFKFKQPTWPGLSSESPKIEIHGDAFTPCGFSNSI	336	
QY	292	LAEKYYTTLHVTPEKGSVASPSNPVDFISQKQDNLDVLHILNVFPQRFESMTFFT	351	
DB	337	-NESNYTTHVTPEPGWSVASFETNM-----IGDYKAIVDKCINVPQGFQFMTVFLT	387	

Qy 352 KNYNQSFQKLLSINESLPDYIKLDKIVYDLDVYHLFYMKLQKK 395
Db 388 -NTDMKFECCLD-----DYKNHRELDVEDYKLYFVIRQ 424

RESULT 2

US-09-949-016-10038
; Sequence 10038, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 10038
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10038

Query Match 22.2%; Score 471; DB 4; Length 348;
Best Local Similarity 30.3%; Pred. No. 1.2e-39;
Matches 115; Conservative 70; Mismatches 138; Indels 56; Gaps 10;

Qy 22 LDSTDAFEGPEKLEIWFPHKKSITT-EKTLRIGMDRWIEILKLVCEVLSMKTKEL 80
Db 15 MEAAHFEFEGTEKLELVWFSRQPDANQSGDLRTIPRSEWDILLKDVQCSIIISVTKTDQ 74
Qy 81 DAFLLSESSLFVFDHKLTKMTCTGTTTLFCLEKLFQIVEQELSFAFTTGGKYKPF--- 137
Db 75 EAYVLSSESMFVSKRRPILKTCGTTLLKALVPLLLKARD-----YSGFDSI 121
Qy 138 -KVFYSRRCLFPCKQAAIHQNWADVDYLNKPFNDGKSYSGVRNDKSNHNLVYVTETDR 196
Db 122 QSFYSRKPKFMSHQYPRNFQEELEFLNAPNGAGYCMGRMN-SDCWLYLTLDPE 180
Qy 197 STPKGKEYIEDDDTFEVLMTLDPPECASKFVCGPEASTTALVEPNEDKGHNLYQMTKN 256
Db 181 S-----RVISQPDQTLLEILMSELDPAVMDQFYM-----KDGVTAKDVTRE 220
Qy 257 TRLDEIVNSAQSDLSFHHDAFAFTPCGYSSNMILAKEYYTLHVTPEKGSYASPEIN 316
Db 221 SGIRDLIPGSVIDATM-----FNPCGYSMNGKSDGTWTHITPEPEFSVSPETN 272
Qy 317 IPVFDISQKQDNLVDLLHILNVFPQREFSMTFTTKYQNSQFKLLSINESLPDYIKLD 376
Db 273 -----LSQTSYD--DLIRKVVVEFKPKFVTTLFVN--QSSKCRTVLASQKIEGFKRLD 323
Qy 377 KIVYDLDVYHLFYMKLQKK 395
Db 324 QCSAMFNDYNFVFTSFAKK 342

RESULT 3

US-09-917-254-54
; Sequence 54, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224(JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254

; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 54
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-917-254-54

Query Match 22.2%; Score 470; DB 4; Length 334;
Best Local Similarity 30.3%; Pred. No. 1.4e-39;
Matches 115; Conservative 69; Mismatches 139; Indels 56; Gaps 10;

Qy 22 LDSTDAFEGPEKLEIWFPHKKSITT-EKTLRIGMDRWIEILKLVCEVLSMKTKEL 80
Db 1 MEAAHFEFEGTEKLELVWFSRQPDANQSGDLRTIPRSEWDILLKDVQCSIIISVTKTDQ 60
Qy 81 DAFLLSESSLFVFDHKLTKMTCTGTTTLFCLEKLFQIVEQELSFAFTTGGKYKPF--- 137
Db 61 EAYVLSSESMFVSKRRPILKTCGTTLLKALVPLLLKARD-----YSGFDSI 107
Qy 138 -KVFYSRRCLFPCKQAAIHQNWADVDYLNKPFNDGKSYSGVRNDKSNHNLVYVTETDR 196
Db 108 QSFYSRKPKFMSHQYPRNFQEELEFLNAPNGAGYCMGRMN-SDCWLYLTLDPE 166
Qy 197 STPKGKEYIEDDDTFEVLMTLDPPECASKFVCGPEASTTALVEPNEDKGHNLYQMTKN 256
Db 167 S-----RVISQPDQTLLEILMSELDPAVMDQFYM-----KDGVTAKDVTRE 206
Qy 257 TRLDEIVNSAQSDLSFHHDAFAFTPCGYSSNMILAKEYYTLHVTPEKGSYASPEIN 316
Db 207 SGIRDLIPGSVIDATM-----FNPCGYSMNGKSDGTWTHITPEPEFSVSPETN 258
Qy 317 IPVFDISQKQDNLVDLLHILNVFPQREFSMTFTTKYQNSQFKLLSINESLPDYIKLD 376
Db 259 -----LSQTSYD--DLIRKVVVEFKPKFVTTLFVN--QSSKCRTVLASQKIEGFKRLD 309
Qy 377 KIVYDLDVYHLFYMKLQKK 395
Db 310 QCSAMFNDYNFVFTSFAKK 328

RESULT 4

US-09-248-796A-19291
; Sequence 19291, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19291
; LENGTH: 753
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19291

Query Match 5.3%; Score 112; DB 4; Length 753;
Best Local Similarity 20.8%; Pred. No. 0.026;
Matches 94; Conservative 63; Mismatches 131; Indels 164; Gaps 24;

Qy 4 TIKELTNHNYIDHE-----LSATLDSDTDAFEGPEKLEIWF 38
Db 131 TLKDM--RNYLDRQKYSNDNLVEFYLSILPGSELGLIGTAIEPTDV--TVKLLDP- 185

Db 705 GLWILGCHNSDFRNRGWTALLKVSSCIPGEGEDDDYLDLEKIFSEDDDY 753

RESULT 9
US-08-558-107-2
; Sequence 2, Application US/08558107
; Patent No. 5910481
; GENERAL INFORMATION:
; APPLICANT: VOORBERG, Johannes J.
; TITLE OF INVENTION: HYBRID PROTEINS WITH MODIFIED ACTIVITY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/558,107
; FILING DATE: 13-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ISACSON, John P.
; REGISTRATION NUMBER: 33,715
; REFERENCE/DOCKET NUMBER: 30472/212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1661 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-558-107-2

Query Match 4.7%; Score 99; DB 2; Length 1661;
Best Local Similarity 20.1%; Pred. No. 2;
Matches 70; Conservative 44; Mismatches 107; Indels 128; Gaps 16;

QY 131 GGYKPKFYVSRRCFLFPCKQAAIHQN-----WADEVLYLNKFPDNGKSYSGVRNDK 183
DB 439 GRKYKKVR-FMAYTDEFTKTRAIQHESGILGPLLYGEVGTLLIIF-----KNQA 488
QY 184 SNHWNLY---VTET---DRSTPKGEYIEDDDTEFEVLMTEL-----D 220
DB 489 SRPNIYPHGITDVRPLYSRRLPKGVKHLKD---FPILPGEIFKYKWTVTVEDGPTKSD 544
QY 221 PECA-----SKFVCGPEASTALVPE-----NEDKGNLGYQMTKNTLDELYVNSAODSDL 272
DB 545 PRCLTRYYSFVNMRDLASGLIGPLLIICYKESVDQGNQIMSDKR--NVILSFVDENR 602
QY 273 SPH-----HDAFAFTPCGYSNNMILAEKYYTTLHVTPEKGSYASFESNIPVFDISQKQD 328
DB 603 SWYLTENIQRLPNPAGVQLE-----DPEFQASNMHSINGVYVDSLQ----- 645
QY 329 NLDVLLH-----ILNVQPRFESMTFTT----- 351
DB 646 -LSVCLHEVAYWYILSIGAQTDFLSVFFSGYTFKHKMNVEDTTLTLPFSGETVFMSEN 704
QY 352 -----KNYQNSFQKLLSINESLP-----DYIKLDKIVYDLDY 385
DB 705 GLWILGCHNSDFRNRGWTALLKVSSCIPGEGEDDDYLDLEKIFSEDDDY 753

RESULT 10
US-09-243-539-2
; Sequence 2, Application US/09243539
; Patent No. 6130203
; GENERAL INFORMATION:
; APPLICANT: VOORBERG, Johannes J.
; TITLE OF INVENTION: HYBRID PROTEINS WITH MODIFIED ACTIVITY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/243,539
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/558,107
; FILING DATE: 13-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: ISACSON, John P.
; REGISTRATION NUMBER: 33,715
; REFERENCE/DOCKET NUMBER: 30472/212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1661 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-243-539-2

Query Match 4.7%; Score 99; DB 3; Length 1661;
Best Local Similarity 20.1%; Pred. No. 2;
Matches 70; Conservative 44; Mismatches 107; Indels 128; Gaps 16;

QY 131 GGYKPKFYVSRRCFLFPCKQAAIHQN-----WADEVLYLNKFPDNGKSYSGVRNDK 183
DB 439 GRKYKKVR-FMAYTDEFTKTRAIQHESGILGPLLYGEVGTLLIIF-----KNQA 488
QY 184 SNHWNLY---VTET---DRSTPKGEYIEDDDTEFEVLMTEL-----D 220
DB 489 SRPNIYPHGITDVRPLYSRRLPKGVKHLKD---FPILPGEIFKYKWTVTVEDGPTKSD 544
QY 221 PECA-----SKFVCGPEASTALVPE-----NEDKGNLGYQMTKNTLDELYVNSAODSDL 272
DB 545 PRCLTRYYSFVNMRDLASGLIGPLLIICYKESVDQGNQIMSDKR--NVILSFVDENR 602
QY 273 SPH-----HDAFAFTPCGYSNNMILAEKYYTTLHVTPEKGSYASFESNIPVFDISQKQD 328
DB 603 SWYLTENIQRLPNPAGVQLE-----DPEFQASNMHSINGVYVDSLQ----- 645
QY 329 NLDVLLH-----ILNVQPRFESMTFTT----- 351
DB 646 -LSVCLHEVAYWYILSIGAQTDFLSVFFSGYTFKHKMNVEDTTLTLPFSGETVFMSEN 704
QY 352 -----KNYQNSFQKLLSINESLP-----DYIKLDKIVYDLDY 385
DB 705 GLWILGCHNSDFRNRGWTALLKVSSCIPGEGEDDDYLDLEKIFSEDDDY 753

RESULT 11

[illegible]

```

RESULT 13
US-09-248-796A-19917
; Sequence 19917, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19917
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-19917

```

	Query Match	4.6%; Score 96.5; DB 4; Length 822;
	Best Local Similarity	18.1%; Pred. No. 1.2;
	Matches	92; Conservative 72; Mismatches 164; Indels 181; Gaps 24;
QY	8	LTHNHYIDHELSSATLDSTDAPEGPEKLLIEWF-FPHKKSIITTEKTLRIGN-----DRWIE 62
Db	288	LIEHN---NKINWYQODDTFEVPKGSEIYAFLHPSSNTDINTSVMSNLAIEMLDDLE 344
QY	63	ILKLVKCEVLMSMKTKELDAPLLSSESLFVFDHKLTMKTGGTTTTTLCLEKLFOLVQEQL 122
Db	345	LTPFAELVGKVLHAWRGDFLINVG---YSHKLS-----NLLQEV 384
QY	123	SWAFRTTQQGKYKP-----FKFYSRRCFLF--PCKQAA-----154
Db	385	NNFF-----QPKRKQDRPESIKFKLLKNFKNGFOVFQGVGYHLQLLNDKLYQQDDK 438
QY	155	-----IHQNWADEV-----DYLNKTFDNCKSYSVG 179
Db	439	IEALEKVTVBDVYQHFTQNTWLQIGFAEVLIGHGNFDPFAQSKQIRDIINESMENVKPMWEK 498
QY	180	RNDKSNHNNLYV---TETDRSTPGKE-----YIEDDETFEVLTATELDPPECASK 226
Db	499	YNEEQFHLOQYVLPNPNTIRIYEPLKDTANINCIEYYIQINTNTDKLRVL-----551
QY	227	FVCGPEASTTALVEPNEDK---GHNLGYOMTKNTRLD-----EIYVNSAQDS-DLSFHH 276
Db	552	----TDLFATIIEPCPDQTRTEQLGYVFPVSGTVLGRTLGRFVLIOSETCDYLQYRI 607
QY	277	DAAFAPTCCGYSSNMILAE---KYYTYL-----HVTPB---KGWS---YASPSFN- 316

608	Db	EEFLVQFGVYNNELSTEDFIKFKHALKNIKLTKLKHLEETVRIWSNIIDGYVDFDSDT	667
317	QY	-----IPVDFISQSQDNLDVLHLNVFQPREPSMT-----FFTQNTQVON	356
668	Db	RQVEILENTKDBELVEFFNTFFIAKSNNTGKIITLKSONPIEFTESKKLHSGIINYLYRN	727
357	QY	QSQFKLLLSINESLPDIKDKIVYDLDDY	385
728	Db	Q-----IEINHEL-----IDNLVKQVDEH	746

RESULT 14
US-08-851-567B-26
Sequence 26, Application US/08851567B
Patent No. 6528484
GENERAL INFORMATION:
APPLICANT: Ensigh, Jerald C
APPLICANT: Bowen, David J
APPLICANT: Petell, James
APPLICANT: Fatig, Raymond
APPLICANT: Schoonover, Sue
APPLICANT: french-Constant, Richard
APPLICANT: Rocheleau, Thomas A.
APPLICANT: Blackburn, Michael B.
APPLICANT: Hey, Timothy D.
APPLICANT: Merlo, Donald J.
APPLICANT: Orr, Gregory L.
APPLICANT: Roberts, Jean L.
APPLICANT: Strickland, James A.
APPLICANT: Guo, Lining
APPLICANT: Ciche, Todd A.
APPLICANT: Sukhapinda, Kitisri
TITLE OF INVENTION: Insecticidal Protein Toxins From Photorhabdus
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSER: Dow AgroSciences Patent Department
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,567B
FILING DATE: 05-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/063,615
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/395,497
FILING DATE: 28-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,255
FILING DATE: 06-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,423
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/705,484
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.93804
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1189 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-851-567B-26

Query Match 4.6%; Score 96.5; DB 4; Length 1189;
 Best Local Similarity 20.4%; Pred. No. 2.1; Indels 133; Gaps 20;
 Matches 88; Conservative 59; Mismatches 151;
 QY 7 ELTNHNYIDHLSATLSDTDAFEGPEKLLBIW-FFPHKKSIITTEKTLRNIGMDRWIB-IL 64
 DB 68 QLFHRAIEGYDGTADSAKPYADEQFLYNWDSFNHRYSTWAGKERLKFYAGYIDPTL 127
 QY 65 KLVKCEV-----LSMKYK-----ELDAFLSSESLFVFDHKLTMKTCGTTTLFCL 111
 DB 128 RLNKTEIFTAFEGISQGLKSELVESKLDYLIISYDTLATDY-ITACQCKDKNTIFFI 186
 QY 112 EKLQIIVEQELSWAF-----RTQGGKYKPKFVFSRRCFLFPCKQAAIHQNWADVDY 165
 DB 187 GR-----TONAPAFYWRKUTLVTDGKLPDQSEWRAI-----NAGISEAYSGHVE- 234
 QY 166 LNKFFDNGKS-----YSVGRNDKSN--HWNLYVTETDRSTPKGEYIE---DDDETPEVLM 216
 DB 235 --PWENKHLHWRFTISKEDKIDFVYKNIWVMSDDYSWASKKILELSTFDYNRVGATG 292
 QY 217 TELDPECASKPVCGPEASTTALVEPNEDKGNLGYQMTKRLDEIYVNSAQSDLSFHH 276
 DB 293 SSSPTEVASQY--GSDAQ-----MNTSDDGTLLIFQ 321
 QY 277 DAFAFTP-----CGYSSNMI-----LAEKYVYTLHVTPEKQWS-----YASFES 315
 DB 322 NAGATPSTGVTLCYDSGNVKNLSSTGSANLSKOYATTKLRMCHGQSYNDNNYCNFTL 381
 QY 316 NIPVFDI-----SQGKQDNLVDLLHILNVFOPREFSMTFTTKYQNSQSFQKLLSINES 368
 DB 382 SINTIETSYGTSSDGKQ-----FTPPSGS-----AIDLH 412
 QY 369 LPDYIKLDKIV 379
 DB 413 LPNYVDLNLALL 423

RESULT 15

US-08-867-941-23
 ; Sequence 23, Application US/08867941
 ; Patent No. 5977337
 ; GENERAL INFORMATION:
 ; APPLICANT: Loosmore, Sheena M
 ; APPLICANT: Du, Run-Pan
 ; APPLICANT: Wang, Quijun
 ; APPLICANT: Yang, Yan-Ping
 ; APPLICANT: Klein, Michel H
 ; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
 ; NUMBER OF SEQUENCES: 67
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sim & McBurney
 ; STREET: 6th Floor, 330 University Avenue
 ; CITY: Toronto
 ; STATE: Ontario
 ; COUNTRY: Canada
 ; ZIP: M5G 1R7
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/867,941
 ; FILING DATE: 03-JUN-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:

NAME: Stewart, Michael I
 REGISTRATION NUMBER: 24,973
 REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 595-1155
 TELEFAX: (416) 595-1163
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 944 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-867-941-23
 Query Match 4.5%; Score 95; DB 2; Length 944;
 Best Local Similarity 18.8%; Pred. No. 2.1;
 Matches 75; Conservative 63; Mismatches 152; Indels 110; Gaps 19;
 QY 5 IKELTNHNYI-DHLSATLSDTDAFEGPEKLLBIWFFPHKKSIITTEKTLRNIGMDRWIEI 63
 DB 376 IRDMTEKQYVGTDEAKKFRDKSGVYDGDPRDGLYFVFN-----IEEWKGD 421
 QY 64 LKLVKCEVLSMKTKKELDAF-----LL-----SESLFVFDHKLTMKTCGT 104
 DB 422 QKLIRGIGLKYSRKTFIDEHRRRRRMGLLYRYENKYSNWDKAVLSFD-KQGVATDNN 480
 QY 105 TTTLFCLEKLFQIIVEQELSWAFRTTQGGKYKPKFVFSRRC-----FLPCKQAAIHQ 157
 DB 481 TLKILNC--AVYPAVD-----KSCRASADKPYSDSDRPHYREQHNVLNASFEKSLKN 531
 QY 158 NWADEVVDYLNKFFDNGKSYSGVGRNDKSNHWNLYVTETDRSTPKGEYIEDDETFEVLM 217
 DB 532 KWTQH--HLTLGFGYDASNAISRPEQLSHNAARISEYSDYTDKDKYLLG----- 579
 QY 218 ELDPKASCKPVCG-PEASTTALVEPNEDKGNLGYQMTKRLDEIYVNSAQSDLSFHH 276
 DB 580 --KPEVVEGSCGYIETLSRKCVPRKINGSNIHISLN-----DRFSIGKYFDFSLGGY 632
 QY 277 DAFAFTPCGVSSNNILAEKYVYTLHVTPEKQWSYASFESNIPVFDISQGKQDNLVDLLHI 336
 DB 633 DRKNFTT--SEELVRSGRYV-----DRSMN-----SGI----- 658
 QY 337 LNVFQP-REFSMTF-FTKYNQNSQFQKLLSINESLPDYIK 374
 DB 659 --VFKNREHESLSYRASSGERTPSFQELFGI-DIYHDYK 695

Search completed: May 11, 2005, 22:53:51
 Job time : 29.1959 secs

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OM protein - protein search, using sw model

Run on: May 11, 2005, 22:36:02 ; Search time 101.041 Seconds
(without alignments)
1515.788 Million cell updates/sec

Title: US-10-732-923-406

Perfect score: 2118

Sequence: 1 MTVTIKELTNHNYIDHELSA.....KIVYDLDYHLYMKLQKKI 396

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2118	100.0	396	8	Adm48038 Polypepti
2	2118	100.0	396	8	AdS43908 Bacterial
3	709.5	33.5	478	8	AdG92091 Fungal S-
4	681	32.2	503	8	Adn20733 Bacterial
5	645	30.5	493	7	Adm07131 Aspergill
6	645	30.5	493	7	Adm07012 Aspergill
7	565	26.7	369	8	Adn19900 Bacterial
8	480	22.7	333	7	AdE60568 Rat Prote
9	480	22.7	333	7	AdD48323 Rat Prote
10	480	22.7	333	7	AdE60572 Rat Prote
11	480	22.7	333	7	AdD48319 Rat Prote
12	471	22.2	347	4	AbB61186 Drosophill
13	471	22.2	348	3	Aab56589 Human pro
14	470	22.2	334	5	Aau84313 Protein A
15	470	22.2	334	7	AdE60574 Human Pro
16	470	22.2	334	7	AdD48325 Human Pro
17	470	22.2	334	7	AdE60570 Human Pro
18	470	22.2	334	7	AdD48321 Human Pro
19	470	22.2	334	8	Adn03708 Antipeori
20	470	22.2	334	8	AdQ8208 Human 912
21	464	21.9	348	4	AbG05997 Novel hum
22	434	20.5	368	8	Adn22644 Bacterial
23	434	20.5	368	8	Adn22643 Bacterial
24	375.5	17.7	366	3	Aag28816 Arabidops
25	372.5	17.6	400	8	Adm48040 Polypepti

26	365	17.2	363	5	AAU79674	Aau79674 Cucurbita
27	365	17.2	363	7	ABG75228	Abg75228 Plant wit
28	365	17.2	363	8	ADP90956	Adp90956 Figleaf g
29	365	17.2	363	8	ADR38366	Adr38366 Fig leaf
30	336	15.9	360	2	AAR75006	Aar75006 Tomato S-
31	294	13.9	366	8	ADM48039	Adm48039 Polypepti
32	269.5	12.7	237	7	ABM73860	Abm73860 DNA clone
33	220.5	10.4	309	7	ABM73938	Abm73938 DNA clone
34	190.5	9.0	215	3	AAG28817	Aag28817 Arabidops
35	173.5	8.2	184	8	ADG66385	Adg66385 Novel hum
36	158	7.5	184	3	AAG28818	Aag28818 Arabidops
37	119.5	5.6	196	4	ABG05996	Abg05996 Novel hum
38	111	5.2	1197	4	ABB58180	Abb58180 Drosophill
39	111	5.2	1197	7	ADJ37903	Adj37903 D melanog
40	110.5	5.2	900	3	AAB18159	Aab18159 Plasmodiu
41	108.5	5.1	585	7	ADC95867	Adc95867 E. faeciu
42	107.5	5.1	749	5	AB904872	Abb04872 LDL recep
43	106.5	5.0	465	2	AAW78921	Aaw78921 Human hae
44	106.5	5.0	1028	4	AAU35923	Aau35923 Helicobac
45	105.5	5.0	655	4	ABG11204	Abg11204 Novel hum

ALIGNMENTS

RESULT 1

ADM48038

ID ADM48038 standard; protein; 396 AA.

XX ADM48038;

DT 03-JUN-2004 (first entry)

DE Polypeptide sequence #88 useful in producing transgenic plants.

XX Yeast; maize; rice; sorghum; thale cress; soybean; wheat; transgenic;

KW osmotic stress; sugar transport; cell cycle pathway; plant height;

KW carbohydrate transport; crop productivity; plant growth;

KW stress resistance; disease resistance; insect resistance; heat tolerance;

KW nitrogen assimilation; water stress tolerance;

KW photosynthetic carbon fixation; virus resistance; gene therapy; gene; ds.

XX Saccharomyces cerevisiae.

XX US2003233670-A1.

XX 18-DEC-2003.

XX 04-DEC-2002; 2002US-00310154.

XX 04-DEC-2001; 2001US-0337358P.

XX (EDGE/) EDGERTON M D.

XX (CHOM/) CHOMET P S.

XX (LACC/) LACCETTI L B.

XX Edgerton MD, Chomet PS, Laccetti LB;

XX WPI; 2004-061374/06.

XX N-PSDB; ADM47670.

XX New polynucleotide, useful for manipulating plant protein quality,
improving plant growth, yield and crop productivity or grain composition
or producing plants with improved properties.

XX Claim 8; SEQ ID NO 456; 144pp; English.

XX The present invention relates to polynucleotide sequences, and the
proteins they encode. The sequences are isolated from a variety of
organisms such as plants (e.g. maize, rice, sorghum, thale cress,
soybean, and wheat), cyanobacteria, bacteria, yeast and other fungi. The
polynucleotide and polypeptide sequences of the invention are useful in
the production of transgenic plants that have improved properties. Also

CC disclosed are methods of producing fertile transgenic plants, preferably
 CC maize, with desired phenotypes. The polynucleotide and polypeptide
 CC sequences are useful for improving plants by providing protection against
 CC osmotic stress, improving altering sugar transport and/or metabolism,
 CC modifying the cell cycle pathway, reducing plant height, modifying
 CC carbohydrate transport, improving crop productivity, improving plant
 CC growth and stress resistance, improving disease resistance, improving
 CC insect resistance, improving cold or heat tolerance, improving nitrogen
 CC assimilation, improving stalk strength, improving water stress tolerance,
 CC improving photosynthetic carbon fixation, improving biotic and abiotic
 CC stress resistance, improving resistance to oxidative stress, providing
 CC increased vigour, reducing senescence, and conferring virus resistance.
 CC The present sequence represents a polypeptide sequence of the invention.
 CC Note: The sequence data for this patent is not provided in the printed
 CC specification but is obtained in electronic format from the USPTO website
 CC at segdata.uspto.gov.

XX SQ Sequence 396 AA;
 Query Match 100.0%; Score 2118; DB 8; Length 396;
 Best Local Similarity 100.0%; Pred. No. 1.1e-186;
 Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTVTIKELTNHNYIDHELSTALDSTDAFEGPEKLEIWFPPHKKSIITKTLRNIGMDRW 60
 DB 1 MTVTIKELTNHNYIDHELSTALDSTDAFEGPEKLEIWFPPHKKSIITKTLRNIGMDRW 60
 QY 61 IEILKLVKCEVLSMKTKELDALLSESSLFVFDHKLTMKTCGTTTTLFCLEKLFQIVEQ 120
 DB 61 IEILKLVKCEVLSMKTKELDALLSESSLFVFDHKLTMKTCGTTTTLFCLEKLFQIVEQ 120
 QY 121 ELSWAFRTTGGKYKPKFYPSRRCFLFPCKQAAIHQNWADVDYLNKFPDNGKSYSGR 180
 DB 121 ELSWAFRTTGGKYKPKFYPSRRCFLFPCKQAAIHQNWADVDYLNKFPDNGKSYSGR 180
 QY 181 NDKSNHNLVYTTDRSTPKGKEYIEDDDTFFVLMTDPECAKVFVCCPEASTTALVE 240
 DB 181 NDKSNHNLVYTTDRSTPKGKEYIEDDDTFFVLMTDPECAKVFVCCPEASTTALVE 240
 QY 241 PNEDKGNLGYQMTKNTRLDEIYVNSAQSDLSFHHDAFAFTPCGYSSNMILAEKYYTTL 300
 DB 241 PNEDKGNLGYQMTKNTRLDEIYVNSAQSDLSFHHDAFAFTPCGYSSNMILAEKYYTTL 300
 QY 301 HVTPEKGSVASPESNIPVFDISQKQDNLVLLHLNVFPQPREFSMTFTTKYQNSQFQ 360
 DB 301 HVTPEKGSVASPESNIPVFDISQKQDNLVLLHLNVFPQPREFSMTFTTKYQNSQFQ 360
 QY 361 KLLSINESLPDYIKLDKIVYDLDYHLFYMKLQKKI 396
 DB 361 KLLSINESLPDYIKLDKIVYDLDYHLFYMKLQKKI 396

RESULT 2
 ADS43908
 ID ADS43908 standard; protein; 396 AA.
 XX AC ADS43908;
 XX DT 02-DEC-2004 (first entry)
 XX DE Bacterial polypeptide #22338.
 XX KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX OS Bacteria.
 XX PN US2003233675-A1.

XX PD 18-DEC-2003.
 XX PF 20-FEB-2003; 2003US-00369493.
 XX PR 21-FEB-2002; 2002US-0360039P.
 XX PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX WPI; 2004-061375/06.
 XX PT New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX PS Claim 1; SEQ ID NO 22338; 122pp; English.
 XX CC The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at segdata.uspto.gov/sequence.html.

XX SQ Sequence 396 AA;
 Query Match 100.0%; Score 2118; DB 8; Length 396;
 Best Local Similarity 100.0%; Pred. No. 1.1e-186;
 Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTVTIKELTNHNYIDHELSTALDSTDAFEGPEKLEIWFPPHKKSIITKTLRNIGMDRW 60
 DB 1 MTVTIKELTNHNYIDHELSTALDSTDAFEGPEKLEIWFPPHKKSIITKTLRNIGMDRW 60
 QY 61 IEILKLVKCEVLSMKTKELDALLSESSLFVFDHKLTMKTCGTTTTLFCLEKLFQIVEQ 120
 DB 61 IEILKLVKCEVLSMKTKELDALLSESSLFVFDHKLTMKTCGTTTTLFCLEKLFQIVEQ 120
 QY 121 ELSWAFRTTGGKYKPKFYPSRRCFLFPCKQAAIHQNWADVDYLNKFPDNGKSYSGR 180
 DB 121 ELSWAFRTTGGKYKPKFYPSRRCFLFPCKQAAIHQNWADVDYLNKFPDNGKSYSGR 180
 QY 181 NDKSNHNLVYTTDRSTPKGKEYIEDDDTFFVLMTDPECAKVFVCCPEASTTALVE 240
 DB 181 NDKSNHNLVYTTDRSTPKGKEYIEDDDTFFVLMTDPECAKVFVCCPEASTTALVE 240
 QY 241 PNEDKGNLGYQMTKNTRLDEIYVNSAQSDLSFHHDAFAFTPCGYSSNMILAEKYYTTL 300
 DB 241 PNEDKGNLGYQMTKNTRLDEIYVNSAQSDLSFHHDAFAFTPCGYSSNMILAEKYYTTL 300

Qy 301 HVTPEKWSYASPNIPVDFISQKQDNLDVLLHILNVFPREFSMFTFTKYNQNSQF 360
 Db 301 HVTPEKWSYASPNIPVDFISQKQDNLDVLLHILNVFPREFSMFTFTKYNQNSQF 360
 Qy 361 KLSINESLSDYIKLDKIVYDLDYHLYFYMKLQKKI 396
 Db 361 KLSINESLSDYIKLDKIVYDLDYHLYFYMKLQKKI 396

RESULT 3
 ADG92091
 ID ADG92091 standard; protein; 478 AA.
 AC ADG92091;
 DT 11-MAR-2004 (first entry)
 XX Fungal S-adenosylmethionine decarboxylase (SPE2).
 DE Rice blast fungus; S-adenosylmethionine decarboxylase; SPE2; antibiotic;
 KW antifungal; polyamine biosynthesis; pathogenicity; fungicide; enzyme.
 XX Magnaporthe grisea.
 OS
 XX US2003224970-A1.
 PN
 XX
 XX 04-DEC-2003.
 XX
 PF 12-MAY-2003; 2003US-00436327.
 PR
 PR 17-MAY-2002; 2002US-0381223P.
 XX
 XX (WAHA/) MAHANTY S.
 PA (HEIN/) HEINIGER R.
 PA (SKAL/) SKALCHUNES A.
 PA (PANH/) PAN H.
 PA (TARP/) TARPEY R.
 PA (SHUS/) SHUSTER J.
 PA (TANZ/) TANZER M M.
 PA (HAME/) HAMER L.
 PA (ADAC/) ADACHI K.
 PA (DEZW/) DEZWAAN T M.
 PA (LOSS/) LO S.
 PA (MONT/) MONTENEGRO-CHAMORRO M V.
 PA (FRAN/) FRANK S.
 PA (DARV/) DARVEAUX B.
 XX
 PI Mahanty S, Heiniger R, Skalchunes A, Pan H, Tarpey R, Shuster J;
 PI Tanzer MM, Hamer L, Adachi K, Dezwaan TM, Lo S;
 PI Montenegro-Chamorro MW, Frank S, Darveaux B;
 XX
 DR WPI; 2004-051922/05.
 DR N-PSDB; ADG92089, ADG92090.
 XX
 PT Identification of test compound as antibiotic e.g. fungicide involves
 PT determining the growth or pathogenicity of fungal organisms having two
 PT forms of a gene involved the polyamine biosynthetic pathway, in the
 PT presence of the compound.
 XX
 PS Claim 41; SEQ ID NO 3; 22pp; English.
 XX
 CC The present invention relates to the isolation of rice blast fungus
 CC (Magnaporthe grisea) S-adenosylmethionine decarboxylase (SPE2), and the
 CC polynucleotide sequences encoding it. Also disclosed is a method for
 CC identifying compounds (e.g. antibiotics, preferably antifungals) that
 CC inhibit SPE2. The enzymes involved in polyamine biosynthesis and
 CC pathogenicity, and the genes encoding the enzymes serve as effective
 CC targets for evaluating antibiotics. The method based on the enzymes and
 CC the genes facilitate screening of effective antibiotics, especially
 CC fungicides. The present sequence represents rice blast fungus SPE2.
 XX
 SQ Sequence 478 AA;

Query Match 33.5%; Score 709.5; DB 8; Length 478;
 Best Local Similarity 35.2%; Pred. No. 2.1e-56;
 Matches 162; Conservative 86; Mismatches 115; Indels 97; Gaps 15;

Qy 14 IDHLSATLDSTDAFEGPEKLLBIWFPFKKSI---TTEKTLRNIGMDRWIELKLVKCE 70
 Db 23 INHDVAQDLDSGAFEGPEKLLWVFPSPSLPLGTGKENGKLSVSPDNVEMLDIVNCK 82
 Qy 71 VLSMKTKELDADFLLSESLFVFDHKLTKMTCTGTTTLFCLKLFQI----- 117
 Db 83 ILSVQSSVVDAYLLSESMFVFPKIIILKTCGTTTLGLAQLLRITAAVDAGFPVNAS 142
 Qy 118 -VEQELSWAFRTTQGGKYKPKFYYSRRCFLPFCQKQAAIHQNWADVDYLNKFPDNGKSY 176
 Db 143 SVEDEKAAA-----TPYRVFYSRKNFLFPDRQGRPHRSWKQEVKYLDSNFEKGSAY 193
 Qy 177 SVGRDNKSNHNLIVYTE-----TDRSTPKGKEYI-----EDDETPEVLMTL 219
 Db 194 MVGKMN-GDHWLYMTSPGSTALTPTTPPAGELMRIPTGLQTAASREDDTLEVLMTDL 252
 Qy 220 DPECASKFVCGPEASTTA-----LVEPNEDKGNLGY 251
 Db 253 DPENAKQFYL-EQASALACKQATLAQOAREEAAALDKAASTDEQLVSEALTTEGHALGT 311
 Qy 252 QMTKNTRLDEIYVNSA-QDSDLSEFHDAFAFTPCGYSSNMIL-----AEKYYT 299
 Db 312 VVSDTCGLSDVYKSKYPDARI---DAYNEFCGFSANGVVPAPPDATCAQGNHYFT 367
 Qy 300 LHVTPEKWSYASPNIPVDFISQKQDNLDVLLHILNVFPREFSMFTFT-KYNQNS 358
 Db 368 VHTTPEPNCYSASFETNVPG---GQNGRETADIIGHVVGIFKPGFESVTLFEGKGRGEN 424
 Qy 359 FQKL---LSINESLPDYIKLDKIVYDLDYHLYFYMKLQKK 395
 Db 425 GTKADQRLRV-DNVPGYRQDKIVHEFDYDYLVRFYQRE 463

RESULT 4
 ADN20733
 ID ADN20733 standard; protein; 503 AA.
 AC ADN20733;
 XX
 XX 02-DEC-2004 (first entry)
 DT
 XX Bacterial polypeptide #3386.
 DE
 XX
 KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 OS Bacteria.
 XX
 XX US2003233675-A1.
 PN
 XX
 PD 18-DEC-2003.
 XX
 PF 20-FEB-2003; 2003US-00369493.
 XX
 PR 21-FEB-2002; 2002US-0360039P.
 XX
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

QY 246 -----GHNLYGQMTKNTLDEIYVNSA-QDSLSFHHDAFAFTPCGYSSNMIL----- 292
Db 312 PPELTTEGHALGTVVSEACGLSSVYKPKYDPSRI-----DAYLFTPCGFGSANGVIPPPEG 367
QY 293 -AEKYYTTLVHTPEKGSYASFSNIPVFDISQKQDNLDVLLHLNLVFPQRFESMTFTT 351
Db 368 KAGTHYFTVHTPEPHCSYASFETNVP---HSQNGQTAGIIKQVVDIFKPGFVSVTLFE 424
QY 352 KNYQNSQFQ-----KLLSIN-----ESLPDYIKLQIVVDLDYHL---FYMKLQKK 395
Db 425 AKPALSQVEDEWKEAKYLAARTAKMEHVEGYRVRDRIVHDLGELYLVFRYERLDWK 482

RESULT 6
ADM07012
ID ADM07012 standard; protein; 493 AA.
XX
AC ADM07012;
XX
XX 20-MAY-2004 (first entry)
XX
XX Aspergillus fumigatus Essential For Growth protein #9.
XX
XX fungicide; gene therapy; Essential For Growth; EFG; fungal infection.
XX
XX Aspergillus fumigatus.
XX
XX WO2003076464-A2.
XX
XX 18-SEP-2003.
XX
XX 13-MAR-2003; 2003WO-IB001374.
XX
XX 13-MAR-2002; 2002US-0363543P.
XX
XX 13-DEC-2002; 2002US-0434407P.
XX
XX (FARB) BAYER CROPSCIENCE SA.
XX
XX (INSP) INST PASTEUR.
XX
XX Grosjean-Cournoyer M, D'enfert CD, Firon A, Villalba F, Lebrun M;
PI Beffa R;
XX
XX WPI; 2003-748377/70.
DR N-PSDB; ADM07010.
XX
XX
XX New nucleic acid encoding an Essential For Growth (EFG) polypeptide,
PT useful for preparing a composition for treating fungal infection caused
PT by Aspergillus fumigatus.
XX
XX Claim 10; SEQ ID NO 27; 259pp; English.
XX
XX The invention relates to a nucleic acid encoding an Essential For Growth
CC (EFG) polypeptide. The nucleic acid is useful for preparing a composition
CC for treating fungal infection caused by Aspergillus fumigatus. This
CC sequence corresponds to a protein of the invention.
XX
XX Sequence 493 AA;
SQ

Query Match 30.5%; Score 645; DB 7; Length 493;
Best Local Similarity 33.9%; Pred. No. 2e-50;
Matches 162; Conservative 80; Mismatches 120; Indels 116; Gaps 17;
QY 14 IDHLSATLSDTAFAEGEKLELWFFPHKKSITTEKT--LRNIGMDRWIEILKVKCEV 71
Db 25 INYEATQDLSDTAFAEGEKLELWFFPHKKSITTEKT--LRNIGMDRWIEILKVKCEV 84
QY 72 LSMKKTDELDAFLSSESLFVFDHKLTKCTGTTTTLFCLEKLFQIVEQBSLWAFRTTQ 131
Db 85 LSIIVSSEVDVAYLLSSESMFWPHKILKTKCTGTTTLLSGLPRILEIA-----ALFG 135
QY 132 GKVK-----PFKVFYSRRCLFPCKQAATHQNWADRVYLNKPFNGKSYSV 178
Db 136 GFPKSTAPSGISVAAAPYRVFYSRKNFLFPDRQGRPHRSWRDEVRTMDKFLNGSAYMI 195

QY 179 GRNDKSNHNLVYTE-----TDRSTPKGK-EYIE-----DDDETEVL 215
Db 196 GKN-GEHWLYLXTEPHMTLTPPTSPCAKTEFTETETKVLSPQGAALQTDSEDTLEVL 254
QY 216 MTBDEPECASKFVCGPEASTALVE-----PNBDK----- 245
Db 255 MTDLDEENAKQFYL---ENATAVAENRYRNSNEKSHGVDFVFNSTSSDISDFSDSGSQL 311
QY 246 -----GHNLYGQMTKNTLDEIYVNSA-QDSLSFHHDAFAFTPCGYSSNMIL----- 292
Db 312 PPELTTEGHALGTVVSEACGLSSVYKPKYDPSRI-----DAYLFTPCGFGSANGVIPPPEG 367
QY 293 -AEKYYTTLVHTPEKGSYASFSNIPVFDISQKQDNLDVLLHLNLVFPQRFESMTFTT 351
Db 368 KAGTHYFTVHTPEPHCSYASFETNVP---HSQNGQTAGIIKQVVDIFKPGFVSVTLFE 424
QY 352 KNYQNSQFQ-----KLLSIN-----ESLPDYIKLQIVVDLDYHL---FYMKLQKK 395
Db 425 AKPALSQVEDEWKEAKYLAARTAKMEHVEGYRVRDRIVHDLGELYLVFRYERLDWK 482

RESULT 7
ADN19900
ID ADN19900 standard; protein; 369 AA.
XX
AC ADN19900;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #2553.
XX
XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
XX US2003233675-A1.
XX
XX 18-DEC-2003.
XX
XX 20-FEB-2003; 2003US-00369493.
XX
XX 21-FEB-2002; 2002US-0360039P.
XX
XX (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
XX WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 2553; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant

CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or by
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX

SQ Sequence 369 AA;

Query Match 26.7%; Score 565; DB 8; Length 369;
 Best Local Similarity 36.1%; Pred. No. 3.2e-43;
 Matches 139; Conservative 75; Mismatches 135; Indels 36; Gaps 13;

QY 14 IDHLSATLSDTAFEGPEKLEIWR-FPHKKSITT-EKT--LRNIGMDRWTEILKLVK 68
 DB 7 VDQENSEEP-NTSFGPEKLELWFSAPIKTNLSAGEKANLGKAVSRNDWDDMLAQ 65
 QY 69 CEVLMMKTKELDAFLSESLFVFDHKLTKMTGTTTTLFCLEKLPQIVEQEELSWAFRT 128
 DB 66 KVLVSVNSEIDAYLLSESSMFVFAHKIILKTCGTTLLASLPRLLEI-----A 115
 QY 129 TQGGKYKPKFVRSRRCFLPCKQAAIHQWAEVDYLNKFPNGKSYSGVRNDKSNHW 188
 DB 116 SSVGDFRPLRIFYSRKNFLYPERQAPHTSWEEBRYLQLFFPSGCSYVVGPTNK-NHWH 174
 QY 189 LYTETDRSTPKGEYEDDDETFEVLMTLDEPCASKF-----VCGPEASTALVEP 241
 DB 175 LFDLADYSL-EDSLDPEDETELEVMTDMPERSQFVAPSLDVVRSARGDDYVREKN 233
 QY 242 NEDKGNHNLGYQMTNTRLDIYVNSAODSLSFHHDFAFTPCGYSSNMILAKEYYYTLH 301
 DB 234 NLSGHLGSYVADESGVRLCSTDKKAVL----DAFQEPFGFSNNMIYKDR-YATIH 288
 QY 302 VTEPKGHSYASPSNIPVFDISQKQNDLVLLHILNVFQPRFESMTFTFTKNVQNSQFK 361
 DB 289 VTFQEHCSYASFETNVSQFGRSISETIE---KTVKTFGANKFCLTLFQAKGASQ--EK 343
 QY 362 LLSIN-ESLPDYIKLDXIVYDLDDY 385
 DB 344 HFSAKLSFSYKKEEFIVDFPGY 368

RESULT 8
 ADE60568
 ID ADE60568 standard; protein; 333 AA.
 XX
 AC ADE60568;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Rat Protein P17708, SEQ ID NO 6478.
 XX
 KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX
 OS Rattus norvegicus.
 XX
 PN W02003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.

XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 DR GENBANK; P17708.
 DR
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 333 AA;

Query Match 22.7%; Score 480; DB 7; Length 333;
 Best Local Similarity 30.9%; Pred. No. 2e-35;
 Matches 117; Conservative 69; Mismatches 137; Indels 56; Gaps 10;
 QY 22 LDSTDAFEGPEKLEIWFPHKKSITT-EKTLNIGMDRWIEILKLVKCVLSNMKTKEL 80
 DB 1 MEAHFPEGTEKLELVWFWSRQSDASQSGDLRTIPRSEMDVLLKQVCSIIISVTKTDKQ 60
 QY 81 DAFELSESLFVFDHKLTKMTGTTTTLFCLEKLPQIVEQEELSWAFRTTQGGYKPF--- 137
 DB 61 EAYVLSESSMFVSKRRFILKTCGTTLLKALVPLLLARD-----YSGFDSI 107
 QY 138 -KVYFRRRCFLFPCKQAAIHQWAEVDYLNKFPNGKSYSGVRNDKSNHNLVVTETDR 196
 DB 108 QSFYGRKNFMKSHQGYPHRNQERIEFLNALFPNGAAYCMGMN-SDCWLYTLDLPE 166
 QY 197 STPKGEYIBDDDETPEVLMTLDEPCASKFVCGPEASTTALVEPNEDKGNHILGYQTKN 256
 DB 167 S-----RVINQPDQTLLEILMSLDPVMDQFYM-----KQGVAKDVRE 206
 QY 257 TRLDIYVNSAODSLSFHHDFAFTPCGYSSNMILAKEYYYTLHVTPEKWSYASPSN 316
 DB 207 SGIRDLPGSVIDA TL-----FNPCGYSMMGMSDGTGYTHITHTPEFESVSVSETN 258
 QY 317 IPVFDISQKQNDLVLLHILNVFQPRFESMTFTFTKNVQNSQFKLLSINESLPDYIKLD 376

Db 259 -----LSQTSYD--DLIRKVEVFKPGKFTVTLFVN--QSSKCRVTLSSPKIDGFKRLD 309
QY 377 KIVYDLDYHLFYMKLOKX 395
Db 310 COSAMFNDYNFVTSFAKK 328
RESULT 9
ADD48323
ID ADD48323 standard; protein; 333 AA.
XX AC ADD48323;
XX 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX XX
DE Rat Protein AAA42105, SEQ ID NO 14021.
XX XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX OS Rattus norvegicus.
XX OS Unidentified.
XX XX
PN WO2003016475-A2.
XX XX
PD 27-FEB-2003.
XX XX
PF 14-AUG-2002; 2002WO-US025765.
XX XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX XX
XX (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX XX
DR WPI; 2003-268312/26.
DR GENBANK; AAA42105.
XX XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX XX
PS Example 1; Page; 1017pp; English.
XX XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic form directly from WIPO at
CC ffp.wipo.int/pub/published_pct_sequences.
XX XX
SQ Sequence 333 AA;
Query Match 22.7%; Score 480; DB 7; Length 333;
Best Local Similarity 30.9%; Pred. No. 2e-35;
Matches 117; Conservative 69; Mismatches 137; Indels 56; Gaps 10;
QY 22 LDSTDAFEGPEKLELWFFPHKKSITT-EKTLNIGMDRWIEILKLVKCEVLNKKTKEL 80
Db 1 MEAHFFEGTEKLELVNFRSQSDASQSGDLTIPRSEWDLVKDVCQSIIVTKTKDQ 60
QY 81 DAFLLSESLFVFDHKLTKTCTGTTTTLFCLEKLFQIVEQELSWAFRTTQGGYKPF-- 137
Db 61 EAVLSESSMFVSKRRFILKTCGTTLLKALVLLKLARD-----YSGFDSI 107
QY 138 -KVYISRRCLFPCKQAAIHQNWADVDYLNKFFDNGKSYSGVGRNDSNHNWLYVTETDR 196
Db 108 QSFYISRRCLFPCKQAAIHQNWADVDYLNKFFDNGKSYSGVGRNDSNHNWLYVTETDR 166
QY 197 STPKGKEYIEDDDETEVELMTLDPDECASKFVCGPEASTTALVEPNEDKGNLGYQWTKN 256
Db 167 S-----RVINQPDQTLLELMSLDPAVMDQFYM-----KQGVTAQVIRE 206
QY 257 TRLDEIYVNSAQSDLSFHHDAFAFTPCGYSSNMILAKEYYYTLHVTPEKGMVSPESN 316
Db 207 SGIRDLIPGSDVATL-----FNPCGYSSNMILAKEYYYTLHVTPEKGMVSPESN 258
QY 317 IPVFDISQKQNDLVLHLILNVQPRFSMTFTTKYQNSQKLLSINESLPDYIKLD 376
Db 259 -----LSQTSYD--DLIRKVEVFKPGKFTVTLFVN--QSSKCRVTLSSPKIDGFKRLD 309
QY 377 KIVYDLDYHLFYMKLOKX 395
Db 310 COSAMFNDYNFVTSFAKK 328
RESULT 10
AD860572
ID AD860572 standard; protein; 333 AA.
XX AC AD860572;
XX XX
DT 29-JAN-2004 (first entry)
XX XX
DE Rat Protein P17708, SEQ ID NO 6482.
XX XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX OS Rattus norvegicus.
XX XX
PN WO2003016475-A2.
XX XX
PD 27-FEB-2003.
XX XX
PF 14-AUG-2002; 2002WO-US025765.
XX XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX XX
XX (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX XX
DR WPI; 2003-268312/26.
DR GENBANK; P17708.
XX XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.

CC cardioactive, immunomodulatory, muscular, vulnery, gastointestinal,
CC nephrotropic, antiinfective, gynaecological and antibacterial activities,
CC and can be used in gene therapy. The prostate cancer antigen
CC polynucleotides may be used for detection of prostate cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The prostate cancer antigens may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
CC AAB57303 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 348 AA;

Query Match 22.2%; Score 471; DB 3; Length 348;
Best Local Similarity 30.3%; Pred. No. 1.4e-34;
Matches 115; Conservative 70; Mismatches 138; Indels 56; Gaps 10;

QY 22 LDSTDAFEGPEKLEIWFPHKKSITT-EKTLRNIGMDRWIEILKLVKCEVLMSKTKEL 80
DB 15 MEAAHFEGETEKLELVFWSRQPPDANQSGDLRTIPRSEWDILKDVQCSIIISVTKTDQ 74
QY 81 DAFLLSSSLFVFDHKLTKMTCTGTTTLFCLEKLFQIVEQELSWAFRTTGGKYKPF--- 137
DB 75 EAYVLSSESMFVSKRRFILTCTGTTLLKALVPLLLARD-----YSGFDSI 121
QY 138 -KVFSRRCFLFPCKQAAIHQWAEVDYLNKFPDNGKYSVGRNDSKNHNLVYVTDTR 196
DB 122 QSPFYSRKFMKPSHOGYPHRNFQEEIEFLNAPFNGAAYCMGRMN-SDCWLYLTLDLDFPE 180
QY 197 STPKGEYIEDDDTEFVLMTELDPEKASFCVCPGEASTTALVPEPNEKGNLGYQMTKN 256
DB 181 S-----RVISQDQTLIELMSELDPVMDQFYM-----KGVTAQVTR 220
QY 257 TRLDEIYVNSAQSDLSFHHDAFAFTPCGYSSNMILAKEYYTLHVTPEKWSYASPE 316
DB 221 SGIRDLIPGVIDATM-----FNPCGYSMNGKSDGTWYTHITPEPEFSYVSPETN 272
QY 317 IPVFDISQKQDNLDVLLHLNVQPREFSMTFTTKYQNSQKLLSINESLPDYIKLD 376
DB 273 -----LSQTSYD--DLIRKVVVEFKPGKFTVTLFVN--QSSKCRVTLASPKIEGFKRLD 323
QY 377 KIVYDLDYHLFYMKLOKK 395
DB 324 QCSAMFNDYNFVFTSFAKK 342

RESULT 14
AAU84313
ID AAU84313 standard; protein; 334 AA.
XX
AC AAU84313;
XX
XX
DT 08-MAY-2002 (first entry)
XX
DE Protein AMD1 differentially expressed in breast cancer tissue.
XX
XX Human; diagnosis of breast cancer; endometrial cancer; breast tumour;
KW MAI; mitotic activity index; cytostatic.
XX
OS Homo sapiens.
XX
XX WO200210436-A2.
XX
XX 07-FEB-2002.
XX
XX 27-JUL-2001; 2001WO-US023642.
XX
XX 28-JUL-2000; 2000US-0222093P.
XX
XX (BGM) BRIGHAM & WOMENS HOSPITAL INC.
PA
PA (BAAK/) BAAK J.
XX

PI Baak J, Mutter GL;
XX WP1: 2002-180084/23.
DR N-PSDB; ABK35533.
XX
PT Diagnosing breast cancer comprises determining expression of nucleic acid
PT molecules or expression products that are differentially expressed in
PT normal and malignant tissue.
XX
PS Claim 37; Page 121-122; 219pp; English.
XX
CC The present invention relates to a method for diagnosing breast cancer in
CC a subject suspected of having endometrial cancer. The method comprises
CC determining the expression of a set of human genes or expression products
CC in an endometrial sample suspected of being cancerous. The human genes of
CC the invention are differentially expressed in breast tumours
CC characterised as high or low MAI (mitotic activity index). These sets of
CC genes can be used to discriminate between high and low MAI breast
CC tumours. The invention also provides DNA and protein microarrays for
CC analysing the expression of the human genes and their protein products.
CC The methods and arrays are useful for the diagnosis and prognosis of
CC endometrial cancer, selecting and monitoring treatment regimes, and
CC identification of compounds useful for the treatment of endometrial
CC cancer. AAU84311-AAU84361 represent the human proteins of the invention
CC that are differentially expressed in breast cancer tissue
XX
SQ Sequence 334 AA;

Query Match 22.2%; Score 470; DB 5; Length 334;
Best Local Similarity 30.3%; Pred. No. 1.7e-34;
Matches 115; Conservative 69; Mismatches 139; Indels 56; Gaps 10;

QY 22 LDSTDAFEGPEKLEIWFPHKKSITT-EKTLRNIGMDRWIEILKLVKCEVLMSKTKEL 80
DB 1 MEAAHFEGETEKLELVFWSRQPPDANQSGDLRTIPRSEWDILKDVQCSIIISVTKTDQ 60
QY 81 DAFLLSSSLFVFDHKLTKMTCTGTTTLFCLEKLFQIVEQELSWAFRTTGGKYKPF--- 137
DB 61 EAYVLSSESMFVSKRRFILTCTGTTLLKALVPLLLARD-----YSGFDSI 107
QY 138 -KVFSRRCFLFPCKQAAIHQWAEVDYLNKFPDNGKYSVGRNDSKNHNLVYVTDTR 196
DB 108 QSPFYSRKFMKPSHOGYPHRNFQEEIEFLNAPFNGAGYCMGRMN-SDCWLYLTLDLDFPE 166
QY 197 STPKGEYIEDDDTEFVLMTELDPEKASFCVCPGEASTTALVPEPNEKGNLGYQMTKN 256
DB 167 S-----RVISQDQTLIELMSELDPVMDQFYM-----KGVTAQVTR 206
QY 257 TRLDEIYVNSAQSDLSFHHDAFAFTPCGYSSNMILAKEYYTLHVTPEKWSYASPE 316
DB 207 SGIRDLIPGVIDATM-----FNPCGYSMNGKSDGTWYTHITPEPEFSYVSPETN 258
QY 317 IPVFDISQKQDNLDVLLHLNVQPREFSMTFTTKYQNSQKLLSINESLPDYIKLD 376
DB 259 -----LSQTSYD--DLIRKVVVEFKPGKFTVTLFVN--QSSKCRVTLASPKIEGFKRLD 309
QY 377 KIVYDLDYHLFYMKLOKK 395
DB 310 QCSAMFNDYNFVFTSFAKK 328

RESULT 15
ADE60574
ID ADE60574 standard; protein; 334 AA.
XX
AC ADE60574;
XX
DT 29-JAN-2004 (first entry)
XX
XX Human Protein P17707, SEQ ID NO 6484.
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW

spared nerve injury; SNI; Chung.

Homo sapiens.

WO2003016475-A2.

27-FEB-2003.

14-AUG-2002; 2002WO-US025765.

14-AUG-2001; 2001US-0312147P.

26-NOV-2001; 2001US-0333347P.

(GEHO) GEN HOSPITAL CORP.

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[illegible]

GENBANK; P17707.

New composition comp

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the generation of a population comprising one or human polynucleotides or a polynucleotide which represents

claimed are a vector comprising

which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIP0 at <http://wipo.int/pub/published> pct sequences.

Sequence 334 AA;

ry Match 22.2%; Score 470; DB 7; Length 334;

conservative 69; mismatches 139; indels 56; gaps 10;

22 LDSTDAFEGPEKLEIWFFPHKKSITT-EKTLRNIGMDRWIEILKLVKCEVLSMKKTKEL 80

1 MEAAHFFEGTEKLEVVWFSRQQPDANQSGDLRTIPRSEWDILLKDVQCSII SVTKTDKQ 60

81 DAFLSESLFVFDHKLTMKTCGTTTLCLEKLFQIVEQELSWAFRTTQGGKYKPF--- 137

61 EAYVLSSESMFVSKRRFILKTCGTTLLKALVPLKLARD-----YSGFDSI 107

138 -KVFSRRRCFLFPCKQAAIHQNWADDEVLYLNKFFDNGKSYSVGRNDKSNHWNLYVTETDR 1966

108 QSFYSRKNFMKPSHQGYPHRNFQEEIEFLNAIFPNGAGYCMGRMN-SDCWYLYTLDFPE 166

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2005, 22:40:28 ; Search time 82.4742 Seconds
(without alignments)
1620.151 Million cell updates/sec

Title: US-10-732-923-408

Perfect score: 2097

Sequence: 1 MAVLSAADSPVSAIGFEGY.....LLCWEEDAMEEKAGYLDE 400

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 1432185

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2097	100.0	400	15	US-10-310-154-458 Sequence 458, App
2	1958.5	93.4	397	16	US-10-767-701-47033 Sequence 47033, A
3	1715	81.8	450	16	US-10-437-963-147033 Sequence 147033,
4	1715	81.8	466	16	US-10-437-963-147475 Sequence 147475,
5	1687.5	80.5	366	15	US-10-310-154-457 Sequence 457, App
6	1632	77.8	395	16	US-10-437-963-142921 Sequence 142921,
7	1632	77.8	554	16	US-10-437-963-142921 Sequence 142921,
8	1626	77.5	305	15	US-10-425-114-39365 Sequence 39365, A
9	1545	73.7	398	16	US-10-767-701-46359 Sequence 46359, A
10	1538	73.3	289	15	US-10-425-114-56960 Sequence 56960, A
11	1517.5	72.4	416	15	US-10-425-114-57997 Sequence 57997, A
12	1517.5	72.4	416	15	US-10-425-114-67343 Sequence 67343, A
13	1515.5	72.3	422	15	US-10-425-114-36776 Sequence 36776, A

14	1474	70.3	276	15	US-10-425-114-69727 Sequence 69727, A
15	1357	64.7	392	16	US-10-437-963-128930 Sequence 128930,
16	1354.5	64.6	395	16	US-10-767-701-46141 Sequence 46141, A
17	997	47.5	187	15	US-10-425-114-57416 Sequence 57416, A
18	954	45.5	181	15	US-10-425-114-57901 Sequence 57901, A
19	933.5	44.5	355	15	US-10-424-599-249854 Sequence 249854,
20	933.5	44.5	355	15	US-10-424-599-249859 Sequence 249859,
21	933.5	44.5	356	15	US-10-425-114-46255 Sequence 46255, A
22	933.5	44.5	356	15	US-10-425-114-46648 Sequence 46648, A
23	933	44.5	173	15	US-10-425-114-56901 Sequence 56901, A
24	933	44.5	363	14	US-10-380-913-4 Sequence 4, Appli
25	919.5	43.8	355	15	US-10-424-599-249855 Sequence 249855,
26	919.5	43.8	360	15	US-10-425-114-43048 Sequence 43048, A
27	919.5	43.8	360	15	US-10-425-114-46323 Sequence 46323, A
28	919.5	43.8	360	15	US-10-425-114-47297 Sequence 47297, A
29	885	42.2	361	15	US-10-424-599-205003 Sequence 205003,
30	872	41.6	331	15	US-10-425-114-71868 Sequence 71868, A
31	831	39.6	156	15	US-10-425-114-47572 Sequence 47572, A
32	693.5	33.1	203	15	US-10-425-114-56490 Sequence 205002,
33	667	31.8	224	15	US-10-424-599-205002 Sequence 205002,
34	611	29.1	113	15	US-10-425-114-56995 Sequence 56995, A
35	576.5	27.5	359	16	US-10-437-963-166485 Sequence 166485,
36	466	22.2	368	15	US-10-369-493-5296 Sequence 5296, Ap
37	466	22.2	368	15	US-10-369-493-5297 Sequence 5297, Ap
38	437.5	20.9	369	15	US-10-369-493-2553 Sequence 2553, Ap
39	428.5	20.4	216	15	US-10-425-114-45581 Sequence 45581, A
40	424	20.2	348	9	US-09-925-300-1167 Sequence 1167, Ap
41	420	20.0	334	15	US-10-341-434-12 Sequence 12, Appl
42	420	20.0	334	15	US-10-341-434-20 Sequence 20, Appl
43	420	20.0	334	15	US-10-341-434-127 Sequence 127, App
44	420	20.0	334	17	US-10-753-267-50 Sequence 50, Appl
45	403	19.2	478	15	US-10-436-327-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-10-310-154-458
; Sequence 458, Application US/10310154
; Publication No. US20030233670A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Chomet, Paul S.
; APPLICANT: Adams, Thomas H
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Agarwal, Ameeta K.
; APPLICANT: Ahrens, Jeffrey E.
; APPLICANT: Ball, James A.
; APPLICANT: Banu, G.
; APPLICANT: Bell, Erin
; APPLICANT: Boddupalli, Raghava
; APPLICANT: Deikman, Jill
; APPLICANT: Deng, Molian
; APPLICANT: Dong, Jinzhao
; APPLICANT: Duff, Stephen M.
; APPLICANT: Galligan, Meghan M.
; APPLICANT: Hinchey, Brenda S.
; APPLICANT: Huang, Shihshien
; APPLICANT: Johnson, G. Richard
; APPLICANT: Jung, Vincent
; APPLICANT: Kretzmer, Keith A
; APPLICANT: Laccetti, Lucille B.
; APPLICANT: Lai, Chao-Qiang
; APPLICANT: Lee, Gary
; APPLICANT: Lin, Jie-Yi
; APPLICANT: Liu, Jingdong
; APPLICANT: Lu, Bin
; APPLICANT: Luethy, Michael M.
; APPLICANT: Lund, Adrian
; APPLICANT: Madson, Linda L.
; APPLICANT: Malloy, Kathleen A.
; APPLICANT: McKiel, Christine L.

APPLICANT: Miller, Philip W.
APPLICANT: Padmavathi, Manchikanti
APPLICANT: Parnell, Laurence D.
APPLICANT: Start, William G.
APPLICANT: Tennesen, Dan
APPLICANT: Vidya, K.R.
APPLICANT: Wang, Haiyun
APPLICANT: Xin, Zhaoguo
APPLICANT: Xu, Nanfei
APPLICANT: Yang, Chunzhi
APPLICANT: Zeng, Xiaoping
APPLICANT: Zhang, Qiang
APPLICANT: Zhao, Yajuan
APPLICANT: Zhou, Li
TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
FILE REFERENCE: 38-15(52796)B
CURRENT APPLICATION NUMBER: US/10/310,154
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,358
PRIOR FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 736
SEQ ID NO 458
LENGTH: 400
TYPE: PRT
ORGANISM: Zea mays
US-10-310-154-458

Query Match 100.0%; Score 2097; DB 15; Length 400;
Best Local Similarity 100.0%; Pred. No. 9.1e-213;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAVLSAADAPSVSAIGFEGYKLEITFSEAPVDPHGRLRAISQAQIDSVLDLART 60
Db 1 MAVLSAADAPSVSAIGFEGYKLEITFSEAPVDPHGRLRAISQAQIDSVLDLART 60
Qy 61 IVSELSNKDFSDSYLSESSLFYPLKIVIKTCGTTKLLTIPRILELAELSMPPLAAVKY 120
Db 61 IVSELSNKDFSDSYLSESSLFYPLKIVIKTCGTTKLLTIPRILELAELSMPPLAAVKY 120
Qy 121 SRGTFFPGAQAPAPHRFSFSEVAALNRYFGGLKSGGNAYVIGDPARPGQKWHVFYATEYP 180
Db 121 SRGTFFPGAQAPAPHRFSFSEVAALNRYFGGLKSGGNAYVIGDPARPGQKWHVFYATEYP 180
Qy 181 EQPMVNLKMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDEPC 240
Db 181 EQPMVNLKMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDEPC 240
Qy 241 GYSNNAIHGSAFSTIHTVTPEDGFSYASYEVMGLDATALSYGDLVKRVLRCFGSPSEFSVAV 300
Db 241 GYSNNAIHGSAFSTIHTVTPEDGFSYASYEVMGLDATALSYGDLVKRVLRCFGSPSEFSVAV 300
Qy 301 TIFGGRHAGTWGKALGAEVYDCNNMVQEQLPGGGLLVYQSFCAAEADAVATSPKSVPHCF 360
Db 301 TIFGGRHAGTWGKALGAEVYDCNNMVQEQLPGGGLLVYQSFCAAEADAVATSPKSVPHCF 360
Qy 361 DGENVESAPPMKDYKLANLLCWEEDADAMEEKAGVLDE 400
Db 361 DGENVESAPPMKDYKLANLLCWEEDADAMEEKAGVLDE 400

RESULT 2
US-10-767-701-47033
Sequence 47033, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 47033
LENGTH: 397
TYPE: PRT
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-C49_367.pgp
US-10-767-701-47033

Query Match 93.4%; Score 1958.5; DB 16; Length 397;
Best Local Similarity 94.2%; Pred. No. 4.2e-198;
Matches 377; Conservative 7; Mismatches 13; Indels 3; Gaps 2;

Qy 1 MAVLSAADAPSVSAIGFEGYKLEITFSEAPVDPHGRLRAISQAQIDSVLDLART 60
Db 1 MAVLSAADAPSVSAIGFEGYKLEITFSEAPVDPHGRLRAISQAQIDSVLDLART 60
Qy 61 IVSELSNKDFSDSYLSESSLFYPLKIVIKTCGTTKLLTIPRILELAELSMPPLAAVKY 120
Db 61 IVSELSNKDFSDSYLSESSLFYPLKIVIKTCGTTKLLTIPRILELAELSMPPLAAVKY 120
Qy 121 SRGTFFPGAQAPAPHRFSFSEVAALNRYFGGLKSGGNAYVIGDPARPGQKWHVFYATEYP 180
Db 121 SRGTFFPGAQAPAPHRFSFSEVAALNRYFGGLKSGGNAYVIGDPARPGQKWHVFYATEYP 180
Qy 181 EQPMVNLKMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDEPC 240
Db 181 EQPMVNLKMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDEPC 240
Qy 241 GYSNNAIHGSAFSTIHTVTPEDGFSYASYEVMGLDATALSYGDLVKRVLRCFGSPSEFSVAV 300
Db 241 GYSNNAIHGSAFSTIHTVTPEDGFSYASYEVMGLDATALSYGDLVKRVLRCFGSPSEFSVAV 300
Qy 301 TIFGGRHAGTWGKALGAEVYDCNNMVQEQLPGGGLLVYQSFCAAEADAVATSPKSVPHCF 360
Db 301 TIFGGRHAGTWGKALGAEVYDCNNMVQEQLPGGGLLVYQSFCAAEADAVATSPKSVPHCF 360
Qy 361 DGENVESAPPMKDYKLANLLCWEEDADAMEEKAGVLDE 400
Db 361 EGVNMEAPP--VDRKLANLLCW-BEVDAMEEKDGVLD 397

RESULT 3
US-10-437-963-147033
Sequence 147033, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 147033
LENGTH: 450
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_475C.1.pgp
US-10-437-963-147033

Query Match 81.8%; Score 1715; DB 16; Length 450;
Best Local Similarity 83.3%; Pred. No. 3.1e-172;
Matches 335; Conservative 21; Mismatches 40; Indels 6; Gaps 4;

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Qy 1 MAVLSAADAPVSAIGFEGYEKRLIEITFSBAPVVDPHGRGLRALSRAQIDSVLDLARCT 60
Db 53 MGVLSSAADPPVSAIGFEGYEKRLIEITFSBAPVVDPHGRGLRALSRAQIDSVLDLARCT 112
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Db 113 IVSELSNKDFDSYVLSSESLFIYSDKIVIKTCGTTKLLLTIPRIELEAELSPLAAVKY 172
Qy 121 SRGTFFIPGAQAPHRFSFSEVAVLNRYFGLKSGGNAYVIGDPAKPGQKWHFYATEYP 180
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Qy 181 EQPMVNLNEMCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDEPC 240
Db 233 EQPMVNLNEMCMTGLDKKACVFFKTSADGHTSCAKEMTKLSGISEIIPEMEICDFDEPC 292
Qy 241 GYSNNAIHGSAFSTIHTVPEDGFSYASVEYVGVFDPASTLAYGDLVKRVLRCFGSPSEFSVAV 300
Db 293 GYSNNAIHGSAFSTIHTVPEDGFSYASVEYVGVFDPASTLAYGDLVKRVLRCFGSPSEFSVAV 352
Qy 301 TIFGGRHAGTGWKALCAEVYDCNNMVQEQLPCGGLLYVQSFCAAE--AVATSPKSVFH 358
Db 353 TIFGGRHAGTGWKALNADAYKCNMVQEQLPCGGLLYVQSFCAAE--DALEENDGVFDE 412
Qy 359 CFGEENVESAPPPMKDYKLANLLCWEEADAMEEKAGVLDE 400
Db 413 CFGEENVESAPPPMKDYKLANLLCWEEADAMEEKAGVLDE 450

RESULT 4
US-10-437-963-147475
; Sequence 147475, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)/B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 147475
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(466)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_479C.1.pap
US-10-437-963-147475

Query Match 81.8%; Score 1715; DB 16; Length 466;
Best Local Similarity 83.3%; Pred. No. 3.2e-172;
Matches 335; Conservative 21; Mismatches 40; Indels 6; Gaps 4;

Qy 1 MAVLSAADAPVSAIGFEGYEKRLIEITFSBAPVVDPHGRGLRALSRAQIDSVLDLARCT 60
Db 69 MGVLSSAADPPVSAIGFEGYEKRLIEITFSBAPVVDPHGRGLRALSRAQIDSVLDLARCT 128
Qy 61 IVSELSNKDFDSYVLSSESLFIYPLKVIKTCGTTKLLLTIPRIELEAELSPLAAVKY 120
Db 129 IVSELSNKDFDSYVLSSESLFIYSDKIVIKTCGTTKLLLTIPRIELEAELSPLAAVKY 188
Qy 121 SRGTFFIPGAQAPHRFSFSEVAVLNRYFGLKSGGNAYVIGDPAKPGQKWHFYATEYP 180
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Db 189 SRGMFIIPSAQAPHRFSFSEVAVLNRYFGLKSGGNAYVIGDPAKPGQKWHFYATQHP 248
Qy 181 EQPMVNLNEMCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDEPC 240
Db 249 EQPMVNLNEMCMTGLDKKACVFFKTSADGHTSCAKEMTKLSGISEIIPEMEICDFDEPC 308
Qy 241 GYSNNAIHGSAFSTIHTVPEDGFSYASVEYVGVFDPASTLAYGDLVKRVLRCFGSPSEFSVAV 300
Db 309 GYSNNAIHGSAFSTIHTVPEDGFSYASVEYVGVFDPASTLAYGDLVKRVLRCFGSPSEFSVAV 368
Qy 301 TIFGGRHAGTGWKALCAEVYDCNNMVQEQLPCGGLLYVQSFCAAE--AVATSPKSVFH 358
Db 369 TIFGGRHAGTGWKALNADAYKCNMVQEQLPCGGLLYVQSFCAAE--DALEENDGVFDE 428
Qy 359 CFGEENVESAPPPMKDYKLANLLCWEEADAMEEKAGVLDE 400
Db 429 CFGEENVESAPPPMKDYKLANLLCWEEADAMEEKAGVLDE 466

RESULT 5
US-10-310-154-457
; Sequence 457, Application US/10310154
; Publication No. US20030233670A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Chomet, Paul S.
; APPLICANT: Adams, Thomas H
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Agarwal, Ameeta K.
; APPLICANT: Ahrens, Jeffrey E.
; APPLICANT: Ball, James A.
; APPLICANT: Banu, G.
; APPLICANT: Bell, Erin
; APPLICANT: Boddupalli, Raghava
; APPLICANT: Deikman, Jill
; APPLICANT: Deng, Molian
; APPLICANT: Dong, Jinzhuo
; APPLICANT: Duff, Stephen M.
; APPLICANT: Galligan, Meghan M.
; APPLICANT: Hinchey, Brenda S.
; APPLICANT: Huang, Shishieh
; APPLICANT: Johnson, G. Richard
; APPLICANT: Jung, Vincent
; APPLICANT: Kretzmer, Keith A.
; APPLICANT: Laccetti, Lucille B.
; APPLICANT: Lai, Chao-Qiang
; APPLICANT: Lee, Gary
; APPLICANT: Lin, Jie-Yi
; APPLICANT: Liu, Jingdong
; APPLICANT: Lu, Bin
; APPLICANT: Luethy, Michael M.
; APPLICANT: Lund, Adrian
; APPLICANT: Madson, Linda L.
; APPLICANT: Malloy, Kathleen A.
; APPLICANT: McKiel, Christine L.
; APPLICANT: Miller, Philip W.
; APPLICANT: Padmavathi, Manchikanti
; APPLICANT: Parnell, Laurence D.
; APPLICANT: Start, William G.
; APPLICANT: Tennesen, Dan
; APPLICANT: Vidya, K.R.
; APPLICANT: Wang, Haiyun
; APPLICANT: Xin, Zhanquo
; APPLICANT: Xu, Nanfei
; APPLICANT: Yang, Chunzhi
; APPLICANT: Zeng, Xiaoping
; APPLICANT: Zhang, Qiang
; APPLICANT: Zhao, Yajuan
; APPLICANT: Zhou, Li
; TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
; FILE REFERENCE: 38-15(52796)B
; CURRENT APPLICATION NUMBER: US/10/310,154
```

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; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,358
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 736
; SEQ ID NO 457
; LENGTH: 366
; TYPE: prt
; ORGANISM: Zea mays
US-10-310-154-457

```

Query Match 80.5%; Score 1687.5; DB 15; Length 366;
Best Local Similarity 85.0%; Pred. No. 1.8e-169;
Matches 328; Conservative 7; Mismatches 20; Indels 31; Gaps 2;

Qy	60	MAVLGAADASPVSALGFGYEGYKRLEITFSEAPVFDVPHGGLRALSRSAQSDSVLDIARCT	60
Db	1	MAVLGAADASPVSALGFGYEGYKRLEITFSEAPVFDVPHGGLRALSRSAQSDSVLDIARCT	1
Qy	120	IVSELSNKDFDSYVLSSESLFIYPLKIVIKTCGGTTKLLLTIPRILELABELSMPLAAVKY	120
Db	59	-----KIVIKTCGGTTKLLLTIPRILELABELSMPLAAVKY	59
Qy	180	SRGTIFPGAQAPAPHRSEFEEVAALNRYFGLGKSGGNAYVIGDPAEPGQKWHFYATEYP	180
Db	94	SRGTIFPGAQAPAPHRSEFEEVAALNRYFGLGKSGGNAYVIGDPAEPGQKWHFYATEYP	94
Qy	240	EQPMVNLNEMCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDQDFEPC	240
Db	154	EQPMVNLNEMCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDQDFEPC	154
Qy	300	GYSMAIHGSAFSTTHVTPEDGFSYASVEVNGLDATALSXGDLVKVRLCGFSPSESVAV	300
Db	214	GYSMAIHGSAFSTTHVTPEDGFSYASVEVNGLDATALSXGDLVKVRLCGFSPSESVAV	214
Qy	360	TIFGGRGAGTGWKGALGAEVDCNNMVEQELPGGGLLYQSFCAAEADVATSPKSFHFCH	360
Db	274	TIFGGRGAGTGWKGALGAEVDCNNMVEQELPGGGLLYQSFCAAEADVATSPKSFHFCH	274
Qy	386	DGENVESAPPMKKDYKLANLLCWEE	386
Db	334	DGENA-----APPAKCDKLANLVCLUE	334

RESULT 6
US-10-437-963-142922
; Sequence 142922, Application US/10437963

```

/ PUBLICATION NO. US20040123343A1
/
/ GENERAL INFORMATION:
/
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Barbazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules
/ TITLE OF INVENTION: Plants and Uses Thereof
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 142922
/ LENGTH: 395
/ TYPE: PRT
/ ORGANISM: Oryza sativa
/ FEATURE:
/
/ OTHER INFORMATION: Clone ID: PAT_MRT4530
/ US-10-437-963-142922

```

Query Match 77.8%; Score 1632; DB 16; Length 395;
Best Local Similarity 79.3%; Pred. No. 1.6e-163;
Matches 314; Conservative 26; Mismatches 46; Indels 10

RESULT 7

US-10-437-963-142921
; Sequence 142921, Application US/10437963
; Publication No. US20040123343A1

```

: GENERAL INFORMATION:
: APPLICANT: La Rosa, Thomas J.
: APPLICANT: Kovalic, David K.
: APPLICANT: Zhou, Yihua
: APPLICANT: Cao, Yongwei
: APPLICANT: Wu, Wei
: APPLICANT: Boukharov, Andrey A.
: APPLICANT: Barbazuk, Brad
: APPLICANT: Li, Ping
: TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
: TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
: FILE REFERENCE: 38-21(53221)B
: CURRENT APPLICATION NUMBER: US(10/437,963
: CURRENT FILING DATE: 2003-05-14
: NUMBER OF SEQ ID NOS: 204966
: SEQ ID NO 142921
: LENGTH: 554
: TYPE: PRT
: ORGANISM: Oryza sativa
: FEATURE:
: OTHER INFORMATION: Clone ID: PAT_MRT4530_43880C.1.pep
: US-10-437-963-142921

```

Query Match 77.8%; Score .1632; DB 16; Length 554;
Best Local Similarity 79.3%; Pred. No. 2.6e-163;
Matches 314; Conservative 26; Mismatches 46; Indels 10; Caps 2;

[illegible]

Query Match	77.8%;	Score 1632;	DB 16;	Length 395;
Best Local Similarity	79.3%;	Pred. No. 1.6e-163;		
Matches 314;	Conservative 26;	Mismatches 46;	Indels 10;	Gaps 2;

QY 181 EQPMVNLNEMCMTGLDKKKACVFFKTNADGNTTCAKMTKLSGISIIPEMEICDFDFEPC 240
DB 252 EQPVTLEMCMTGLDKKKASVFFKTSADGHTTVAKEMTKLSGISIIPEMEICDFDFEPC 311
QY 241 GYSMAIHGSAFSTIHTVTPEDGFSYASVEVWGLDATALSYGDLVKRVLRCFGSFSVAV 300
DB 312 GYSMAIHGSAFSTIHTVTPEDGFSYASVEVWGLDATALSYGDLVKRVLRCFGSFSVAV 371
QY 301 TIFGGRHAGTGWKALGAEVYDCNNMVQEQLPGGGLLVYQSFCAAEADAVATSPKSVPHCF 360
DB 372 TIFGGRHAGTGWKALGAEVYDCNNMVQEQLPGGGLLVYQSFCAAEADAVATSPKSVPHCF 431
QY 361 DGENVESAPPMKKOYKLANLLCWEEADAMEEKAG 396
DB 432 ADENTEKAGK-----MEALYWEED--DAVEEIDG 457

RESULT 8
US-10-425-114-39365
; Sequence 39365, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 39365
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700074853_FLI.pbp
US-10-425-114-39365

Query Match 77.5%; Score 1626; DB 15; Length 305;
Best Local Similarity 100.0%; Pred. No. 4.5e-163;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 KLLTTTPIRILELAELSMPPLAAVKYSGTTFPGQAQAPAPHRFSFSEVAAALNRYFGGLKSG 155
DB 1 KLLTTTPIRILELAELSMPPLAAVKYSGTTFPGQAQAPAPHRFSFSEVAAALNRYFGGLKSG 60
QY 156 GNAYVIGDPAAPGQKWHVFYATEYPEOPMVNLEMCMTGLDKKKACVFFKTNADGNTTCAK 215
DB 61 GNAYVIGDPAAPGQKWHVFYATEYPEOPMVNLEMCMTGLDKKKACVFFKTNADGNTTCAK 120
QY 216 EMTKLSGISIIPEMEICDFDFEPCGYSMAIHGSAFSTIHTVTPEDGFSYASVEVWGLDA 275
DB 121 EMTKLSGISIIPEMEICDFDFEPCGYSMAIHGSAFSTIHTVTPEDGFSYASVEVWGLDA 180
QY 276 TALSYGDLVKRVLRCFGSFSFSAVATTIFGGRHAGTGWKALGAEVYDCNNMVQEQLPGGG 335
DB 181 TALSYGDLVKRVLRCFGSFSFSAVATTIFGGRHAGTGWKALGAEVYDCNNMVQEQLPGGG 240
QY 336 LLVYQSFCAAEADAVATSPKSVPHCFDGENVESAPPMKKOYKLANLLCWEEADAMEEKA 395
DB 241 LLVYQSFCAAEADAVATSPKSVPHCFDGENVESAPPMKKOYKLANLLCWEEADAMEEKA 300
QY 396 GVLDE 400
DB 301 GVLDE 305

RESULT 9
US-10-767-701-46359

; Sequence 46359, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 46359
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CL511_1.pbp
US-10-767-701-46359

Query Match 73.7%; Score 1545; DB 16; Length 398;
Best Local Similarity 76.5%; Pred. No. 2.6e-154;
Matches 302; Conservative 36; Mismatches 47; Indels 10; Gaps 3;

QY 1 MAVLSAADAS--EVSAGFEGYKRLKLEITFSEAPVFPVDPHGRGLRALSRQIDSVLDLAR 58
DB 1 MAVLQVAAAAPPVSAIGFEGYKRLKLEITFSEAPVFPADPNRGLRALSRQIDSVLDLAR 60
QY 59 CTIVSELNKPDSYVLSSESLFIYPLKVIKTCGTTKLLTTPRILELAELSMPPLAAV 118
DB 61 CTIVSELNKPDSYVLSSESLFIYPLKVIKTCGTTKLLTTPRILELAELSMPPLAAV 120
QY 119 KYSRGTFIPGAQAPAPHRFSFSEVAAALNRYFGGLKSGGNAYVIGDPAAPGQKWHVFYATE 178
DB 121 KYSRGTFIPGAQAPAPHRFSFSEVAAALNRYFGGLKSGGNAYVIGDPAAPGQKWHVFYATE 180
QY 179 YPEQPMVNLNEMCMTGLDKKKACVFFKTNADGNTTCAKMTKLSGISIIPEMEICDFDFE 238
DB 181 HPEEPVVTLEMCMTGLDKKKASVFFKTSADGNTTCAKMTKLSGISIIPEMEICDFDFE 240
QY 239 PCGYSMAIHGSAFSTIHTVTPEDGFSYASVEVWGLDATALSYGDLVKRVLRCFGSFSV 298
DB 241 PCGYSMAIHGSAFSTIHTVTPEDGFSYASVEVWGLDATALSYGDLVKRVLRCFGSFSV 300
QY 299 AVTIFGGRHAGTGWKALGAEVYDCNNMVQEQLPGGGLLVYQSFCAAEADAVATSPKSVPH 358
DB 301 AVTIFGGRHAGTGWKALGAEVYDCNNMVQEQLPGGGLLVYQSFCAAEADAVATSPKSVPH 360
QY 359 CPDGENVESAPPMKKOYKLANLLCWEEADAMEE 393
DB 361 DFAGDIVKPG-----DSGEADGPCW--EADAVDE 387

RESULT 10
US-10-425-114-56960
; Sequence 56960, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 56960
; LENGTH: 289
; TYPE: PRT

```
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17089E06_FLI.pep
US-10-425-114-56960

Query Match      73.3%; Score 1538; DB 15; Length 289;
Best Local Similarity 99.3%; Pred. No. 8.7e-154;
Matches 287; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 112 SMPAAVYKSRGTIFPGAQAPHRFSFEEVAALNRYFGGLKSGGNAYVIGDPAAPGQKW 171
DB 1 SMPAAVYKSRGTIFPGAQAPHRFSFEEVAALNRYFGGLKSGGNAYVIGDPAAPGQKW 60

QY 172 HVFYATEYPEQPMVNLNEMCTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIPEME 231
DB 61 HVFYATEYPEQPMVNLNEMCTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIPEME 120

QY 232 ICDFDPEPCGYSMNAIHGSAFSTIHVTPEDGFSYASVEVMGLDATALSYGDLVKRVLRCF 291
DB 121 ICDFDPEPCGYSMNAIHGSAFSTIHVTPEDGFSYASVEVMGLDATALSYGDLVKRVLRCF 180

QY 292 GPSEFSVAVTIFGGRGHAGTWKALGAEVYDCNNMVEQELPGGGLLVYQSFCAAEADAVAT 351
DB 181 GPSEFSVAVTIFGGRGHAGTWKALGAEVYDCNNMVEQELPGGGLLVYQSFCAAEADAVAT 240

QY 352 SPKSVFHCFCGDNVESAPPMPKKDYKLANLLCWEEDAMEEKAGVLDE 400
DB 241 SPKSVFHCFCGDNVESAPPMPKKDYKLANLLCWEEDAMEEKAGVLDE 289

RESULT 11
US-10-425-114-57997
; Sequence 57997, Application US/10425114
; Publication No. US20040034889A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 57997
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17023A12_FLI.pep
US-10-425-114-57997

Query Match      72.4%; Score 1517.5; DB 15; Length 416;
Best Local Similarity 74.8%; Pred. No. 2.2e-151;
Matches 297; Conservative 29; Mismatches 52; Indels 19; Gaps 3;

QY 1 MAVLSAADASPVSAGIFGEGYEKLEITFSAPVFDPHGRGLRALSAQAIDSVLDLACT 60
DB 24 MAVLQAAAPPVSVIGFEGEKELEISFSEAPVLADPSGRLRALSAQAIDSVLDLACT 83

QY 61 IVSELSNKDFSDSVLSESSLFYPLKIVIKTCGTTKLLLTIPRILELAELSMPPLAAVKY 120
DB 84 IVSELSNDDFSDSVLSESSLFYVPYKIVIKTCGTTKLLLAIPRILELAELLPLAAVKY 143

QY 121 SRGTFFPGAQAPHRFSFEEVAALNRYFGGLKSGGNAYVIGDPAAPGQKHVYATEYP 180
DB 144 SRGTFFPGAQAPHRFSFEEVAALNRYFGGLKSGGNAYVIGDPAAPGQKHVYAAEHP 203

QY 181 EQPMVNLNEMCTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIPEMEICDFDEPC 240
DB 204 EEPVVTLEMCMTGLDKKASVFFKTTADGYSLCAKEMTKLSGISEIPEMEICDFDEPC 263

QY 241 GYSNNAIHGSAFSTIHVTPEDGFSYASVEVMGLDATALSYGDLVKRVLRCFCGSEFSVAV 300
DB 264 GYSNNAIHGSAFSTIHVTPEDGFSYASVEVMGLDATALSYGDLVKRVLRCFCGTEFSVTV 323

QY 301 TIFGGRGHAGTWKALGAEVYDCNNMVEQELPGGGLLVYQSFCAAEADAVATSPKSVFHC 360
DB 324 TIFGDRNDAKTGTLDAEAYACSNMVEQVLPFGGLLIYOSFTVTAETTHGSPRSVLHDF 383

QY 361 DGENV-----ESAPPMPKKDYKLANLLCWEEDAMEE 393
DB 384 AGDIVKNRSESDAP-----W--EADAVDE 405
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DB 204 EEPVVTLEMCMTGLDKKASVFFKTTADGYSLCAKEMTKLSGISEIPEMEICDFDEPC 263
QY 241 GYSNNAIHGSAFSTIHVTPEDGFSYASVEVMGLDATALSYGDLVKRVLRCFCGSEFSVAV 300
DB 264 GYSNNAIHGSAFSTIHVTPEDGFSYASVEVMGLDATALSYGDLVKRVLRCFCGTEFSVTV 323
QY 301 TIFGGRGHAGTWKALGAEVYDCNNMVEQELPGGGLLVYQSFCAAEADAVATSPKSVFHC 360
DB 324 TIFGDRNDAKTGTLDAEAYACSNMVEQVLPFGGLLIYOSFTVTAETTHGSPRSVLHDF 383
QY 361 DGENV-----ESAPPMPKKDYKLANLLCWEEDAMEE 393
DB 384 AGDIVKNRSESDAP-----W--EADAVDE 405

RESULT 12
US-10-425-114-67343
; Sequence 67343, Application US/10425114
; Publication No. US20040034889A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 67343
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB4767-001-F3_FLI.pep
US-10-425-114-67343

Query Match      72.4%; Score 1517.5; DB 15; Length 416;
Best Local Similarity 74.8%; Pred. No. 2.2e-151;
Matches 297; Conservative 29; Mismatches 52; Indels 19; Gaps 3;

QY 1 MAVLSAADASPVSAGIFGEGYEKLEITFSAPVFDPHGRGLRALSAQAIDSVLDLACT 60
DB 24 MAVLQAAAPPVSVIGFEGEKELEISFSEAPVLADPSGRLRALSAQAIDSVLDLACT 83

QY 61 IVSELSNKDFSDSVLSESSLFYPLKIVIKTCGTTKLLLTIPRILELAELSMPPLAAVKY 120
DB 84 IVSELSNDDFSDSVLSESSLFYVPYKIVIKTCGTTKLLLAIPRILELAELLPLAAVKY 143

QY 121 SRGTFFPGAQAPHRFSFEEVAALNRYFGGLKSGGNAYVIGDPAAPGQKHVYATEYP 180
DB 144 SRGTFFPGAQAPHRFSFEEVAALNRYFGGLKSGGNAYVIGDPAAPGQKHVYAAEHP 203

QY 181 EQPMVNLNEMCTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIPEMEICDFDEPC 240
DB 204 EEPVVTLEMCMTGLDKKASVFFKTTADGYSLCAKEMTKLSGISEIPEMEICDFDEPC 263

QY 241 GYSNNAIHGSAFSTIHVTPEDGFSYASVEVMGLDATALSYGDLVKRVLRCFCGSEFSVAV 300
DB 264 GYSNNAIHGSAFSTIHVTPEDGFSYASVEVMGLDATALSYGDLVKRVLRCFCGTEFSVTV 323

QY 301 TIFGGRGHAGTWKALGAEVYDCNNMVEQELPGGGLLVYQSFCAAEADAVATSPKSVFHC 360
DB 324 TIFGDRNDAKTGTLDAEAYACSNMVEQVLPFGGLLIYOSFTVTAETTHGSPRSVLHDF 383

QY 361 DGENV-----ESAPPMPKKDYKLANLLCWEEDAMEE 393
DB 384 AGDIVKNRSESDAP-----W--EADAVDE 405
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RESULT 13
US-10-425-114-36776
; Sequence 36776, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 36776
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3136-020-E2_FLI.pep
US-10-425-114-36776

Query Match      72.3%; Score 1515.5; DB 15; Length 422;
Best Local Similarity 74.7%; Pred. No. 3.7e-151;
Matches 298; Conservative 31; Mismatches 49; Indels 21; Gaps 4;

QY 1 MAVLSAADAS--PVSAIGFEGYKRLIETPSEAPVFDVPHGRGLRALSRAQIDSVLDLAR 58
DB 28 MAVLVAAAAPPVSVIGFEGFKRLIETPSEAPVLDPSGRGLRALSRAQIDSVLDLAR 87
QY 59 CTIVSELNKFDSYVLSSESLFYPIKIVIKTCGTTKLLTTPRILELAELSMPAAV 118
DB 88 CTIVSELNEDFDSYVLSSESLFYPIKIVIKTCGTTKLLTTPRILELAELSMPAAV 147
QY 119 KYSRGTFIFPGAQAPAPHRFSFSEVAALNRYFGGLKSGGNAYVIGDPPARPGQKWHVYATE 178
DB 148 KYSRGTFIFPEAQPSFHKFADAEVFLNFRFFGLKSGGNAYVIGDSAKFGQKWHVYAAE 207
QY 179 YFPQPMVNLKMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFPE 238
DB 208 HPEEPVTVLEMCMTGDKKKASVFFKTTADGYSILCAKEMTKLSGISEIIPMEICDFPE 267
QY 239 PCGYSNATHGSFSTHVTPEDFGSYASVEVMGLDATALSYGDLVKRVLRCFPGSEFSV 298
DB 268 PCGYSNVAHGPALSTHVTPEDFGSYASVEVMGNFPGSFYSGDLVKRVLRCFPGTEFSV 327
QY 299 AVTIFGGRHAGTWKALGAEVYDCNNMVEQELPGGGLLVYQSFCAAEADAVATSPKSVFH 358
DB 328 AVTIFGDRNAGTWKTLDAEAYACSNMVEQVLPFGGLLIYQSFVTAETHGSPRSVLH 387
QY 359 CFQGENV----ESAPPMKKDYKLANLLCWEEADAMEE 393
DB 388 DFAGDIVKRNESDAP-----W--EADAVDE 411

RESULT 14
US-10-425-114-69727
; Sequence 69727, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114

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; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 69727
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17199H04_FLI.pep
US-10-425-114-69727

Query Match      70.3%; Score 1474; DB 15; Length 276;
Best Local Similarity 99.3%; Pred. No. 4.8e-147;
Matches 274; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 125 FIFPGAQAPAPHRFSFSEVAALNRYFGGLKSGGNAYVIGDPPARPGQKWHVYATEYEQPM 184
DB 1 FIFPGAQAPAPHRFSFSEVAALNRYFGGLKSGGNAYVIGDPPARPGQKWHVYATEYEQPM 60
QY 185 VNLEMCMTGLDKKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFPEPCGYSM 244
DB 61 VNLEMCMTGLDKKKASVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFPEPCGYSM 120
QY 245 NAIHGSFSTHVTPEDFGSYASVEVMGLDATALSYGDLVKRVLRCFPGSEFSVAVTIFG 304
DB 121 NAIHGSFSTHVTPEDFGSYASVEVMGLDATALSYGDLVKRVLRCFPGSEFSVAVTIFG 180
QY 305 GRGHAGTWKALGAEVYDCNNMVEQELPGGGLLVYQSFCAAEADAVATSPKSVFHCDFGEN 364
DB 181 GRGHAGTWKALGAEVYDCNNMVEQELPGGGLLVYQSFCAAEADAVATSPKSVFHCDFGEN 240
QY 365 VESAPPMKKDYKLANLLCWEEADAMEEKAGVLDE 400
DB 241 VESAPPMKKDYKLANLLCWEEADAMEEKAGVLDE 276

RESULT 15
US-10-437-963-128930
; Sequence 128930, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 128930
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_31236C.1.pep
US-10-437-963-128930

Query Match      64.7%; Score 1357; DB 16; Length 392;
Best Local Similarity 67.6%; Pred. No. 2e-134;
Matches 267; Conservative 47; Mismatches 71; Indels 10; Gaps 5;

QY 4 LSAAD---ASPVSAIGFEGYKRLIETPSEAPVFDVPHGRGLRALSRAQIDSVLDLARCT 60
DB 3 MSLADWSGAPASPIGFEYKRLIETLSDAPVFDVPCGGLRALSREQIDSLDLAKCT 62
QY 61 IVSELSNKFDSYVLSSESLFYPIKIVIKTCGTTKLLTTPRILELAELSMPAAV 120
DB 63 IVSHLSNKFDSYVLSSESLFYPIKIVIKTCGTTKLLTTPRILELAELSMPAAV 122

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QY 121 SRGTFIPGAQAPHPSEEEVAALNRYEGGLKSGGNAYVIGDPARPQOKWHVYATEYP 180
Db 123 SRGMFIPGAQSPHRSFLEEVSVLNSFFGGLKSGGNAYVIGDAFKPKKWHVYATEEP 182
QY 181 EQPMVNLWCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFEPC 240
Db 183 EQPMVNLWCMTGLDAKAEVFFKSTDSGSSAKEMTFSGISEIIPEMEICDFDFEPC 242
QY 241 GYSMNAIHGSAFSTIHTVTPEDGFSYASYEVMGLDATALSYGDLVKRVLRCFGPSEFSVAV 300
Db 243 GYSMNGIYGPAVSTIHTVTPEDGFSYASYEAMNFPSSLVYDDLKVKLACFCPSDFSVA 302
QY 301 TIFGGRGHACTWGKALGAEVYDCNNVVEQLPGGGLLVYQSFCAAEADAVATSPKSVFHC 360
Db 303 TIFGGRGHGFAKSWAKGAEVDSYMCDDLVQELPGGGLVYQSFCAAEADAVATSPKSV 358
QY 361 DGENVESAPPPMKDYKLANLLCWESEADAMEEKA 395
Db 359 DGNWSDGA-EMVAKSKEMS--VCWEGEKAACKDA 390

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Search completed: May 11, 2005, 22:57:58
Job time : 83.4742 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2005, 22:39:42 ; Search time 26.4605 Seconds
(without alignments)
1128.461 Million cell updates/sec

Title: US-10-732-923-408
Perfect score: 2097
Sequence: 1 MAVLSAADSPVSAIGFEGY.....LLCWEEDAMBEKAGVLDE 400

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCRUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	424	20.2	348	4	US-09-949-016-10038 Sequence 10038, A
2	420	20.0	334	4	US-09-917-254-54 Sequence 54, Appl
3	406.5	19.4	424	4	US-09-248-796A-18169 Sequence 18169, A
4	101.5	4.8	350	4	US-09-902-540-11867 Sequence 11867, A
5	100.5	4.8	410	4	US-09-010-877-2 Sequence 2, Appl
6	94	4.5	1165	1	US-07-828-788A-14 Sequence 14, Appl
7	94	4.5	1165	1	US-08-356-034-4 Sequence 4, Appl
8	94	4.5	1165	3	US-08-933-891-4 Sequence 4, Appl
9	94	4.5	1165	4	US-09-521-344-4 Sequence 4, Appl
10	94	4.5	1165	4	US-09-837-961A-4 Sequence 4, Appl
11	94	4.5	1165	5	PCT-US92-11337-14 Sequence 14, Appl
12	94	4.5	1165	6	5188960-4 Patent No. 5188960
13	94	4.5	1165	6	5188960-4 Patent No. 5188960
14	91.5	4.4	270	2	US-08-773-368-1 Sequence 1, Appl
15	91.5	4.4	270	3	US-09-199-887-1 Sequence 1, Appl
16	91.5	4.4	502	4	US-09-489-039A-13971 Sequence 13971, A
17	91	4.3	1165	3	US-09-176-320-6 Sequence 6, Appl
18	89.5	4.3	621	4	US-09-537-120-2 Sequence 2, Appl
19	89	4.2	288	4	US-09-270-767-43786 Sequence 43786, A
20	89	4.2	2559	4	US-09-902-540-16112 Sequence 16112, A
21	87.5	4.2	499	4	US-09-543-681A-6892 Sequence 6892, Ap
22	87.5	4.2	856	4	US-09-328-352-7255 Sequence 7255, Ap
23	87	4.1	833	4	US-09-583-110-4098 Sequence 4098, Ap
24	87	4.1	862	4	US-09-107-433-3190 Sequence 3190, Ap
25	86	4.1	795	3	US-07-741-453A-55 Sequence 55, Appl
26	85	4.1	568	4	US-09-902-540-9948 Sequence 9948, Ap
27	85	4.1	634	4	US-09-248-796A-19513 Sequence 19513, A

28	85	4.1	662	4	US-09-543-681A-7467 Sequence 7467, Ap
29	85	4.1	833	2	US-08-844-086-2 Sequence 2, Appl
30	85	4.1	833	3	US-09-018-211-2 Sequence 2, Appl
31	85	4.1	1472	4	US-09-032-438C-119 Sequence 119, App
32	84.5	4.0	866	4	US-09-134-000C-5066 Sequence 5066, Ap
33	84.5	4.0	850	4	US-09-515-181A-3 Sequence 3, Appl
34	84	4.0	331	4	US-09-710-279-874 Sequence 874, App
35	84	4.0	331	4	US-09-710-279-2244 Sequence 2244, Ap
36	84	4.0	342	3	US-09-134-001C-5198 Sequence 5198, Ap
37	84	4.0	607	2	US-08-472-534-5 Sequence 5, Appl
38	84	4.0	607	4	US-09-583-110-4651 Sequence 4651, Ap
39	84	4.0	612	4	US-09-107-433-3621 Sequence 3621, Ap
40	83.5	4.0	766	4	US-09-463-238-6 Sequence 6, Appl
41	82.5	3.9	481	3	US-09-537-357-7 Sequence 7, Appl
42	82.5	3.9	1054	4	US-09-693-542-87 Sequence 87, Appl
43	82	3.9	321	4	US-09-498-520A-18 Sequence 18, Appl
44	81	3.9	251	4	US-09-270-767-48514 Sequence 48514, A
45	81	3.9	308	4	US-09-902-540-14965 Sequence 14965, A

ALIGNMENTS

RESULT 1
US-09-949-016-10038
; Sequence 10038, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10038
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10038

Query Match	20.2%	Score 424;	DB 4;	Length 348;
Best Local Similarity	36.9%	Pred. No. 3.5e-39;		
Matches 109;	Conservative 48;	Mismatches 114;	Indels 24;	Gaps 9;
QY	17	FEYKRLITFSEAVFVDPHGRGRALSRAGIDSVLDRCTIVSELNKNQDFDSVLS	76	
Db	21	FEGETLELWFWRQOPDANQSGDLRTIPRSEWDILLKDVQCSIIIVTKDQEAIVLS	80	
QY	77	ESSLIYPLKIVTKCTGTTKLLTIPRIILELAELS--WPLAAVKYSGCTFIPEGAPAP	134	
Db	81	ESSMFYKRRFILTKTCGTTLLKALVPLKLDYSGFDSIQFFSRKRMKPSHQGY	140	
QY	135	HRFSFEVAAALNRYFGGLKSGGNAYVIGOPARQKQWHVFYATEYPE-----OPMVNLEM	189	
Db	141	HRNFQEIIFLNAIF-----PNGAAYCMG---RWNDCWLYTLDPFSRVISQDQTL	193	
QY	190	CMTGLDKKXACVFEKTNADGNTTCAKMTKLSIGSIIEPMEICDFEPFCGYSMAIHG	249	
Db	194	LMSELDPAVMDQPYM--KDGVT--AKDVTRESGIRDLIPGSDVATMNFPCGYSNMGKS	249	
QY	250	-SAFSIHTHTPEFCFSYASVEVMGLDATALSYGLVKRVLCFCGSEFSVAVIF	303	
Db	250	DGTWTHITHTPEFSYVSFET---NLSQTSYDLDLRKVVVEPKPGKF--VTTLF	299	

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RESULT 2
US-09-917-254-54
; Sequence 54, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224(JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 54
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-917-254-54

Query Match      20.0%; Score 420; DB 4; Length 334;
Best Local Similarity 36.6%; Pred. No. 9.4e-39;
Matches 108; Conservative 48; Mismatches 115; Indels 24; Gaps 9;

QY 17 FEGYKRLTTFSEAPVFDVPHGRGLRALSRQAIDSVLDLACTIVSELSNKKDFDSYVLS 76
DQ 7 FEGTEKLEVFVRQPPDANQSGDLRTIPRSEWDLKKDVOCSIIISVTKTDQEAAYVLS 66
QY 77 ESSLFTYPLKIVTKTCTKLLTIPRILELAELS--MPLAAVKYSRGTFFIFPGAQAP 134
DQ 67 ESSMVFVKRFFIKTCTTLLKALVPLKLDYSGFDSIQFFYSRKNFMPKPSHQY 126
QY 135 HRSFSEVAALNRYFGKSGNAYVIGDPARFGQKWHVFYATEYPE-----QPMVNLEM 189
DQ 127 HRNFQEIPLNAIF----PNGAGYCMG---RNSDCWLYTLDFPESRVISQPDQLEI 179
QY 190 CMTGLDKKACVFPKNADGNTTCAKEMTKLSGISEIIPMEICDFDFPEPCGYSMAIHG 249
DQ 180 LMSGLDPAVMDQYFM--KDGVT--AKDVTRESGIRDLIPGSVIDATMFNPNCGYSMNGMS 235
QY 250 -SAFSTHTVTPGFSYASVEVMGLDATALSYGLVKVLRFCGSPSEFSVAATIF 303
DQ 236 DGTWTHITPEEFSVSFET---NLSQTSYDILIRKVVFPKPGF--VTTLF 285

RESULT 3
US-09-248-796A-18169
; Sequence 18169, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18169
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18169

Query Match      19.4%; Score 406.5; DB 4; Length 424;
Best Local Similarity 32.2%; Pred. No. 4.8e-37;
Matches 110; Conservative 58; Mismatches 99; Indels 75; Gaps 12;

QY 13 SAIGFEGYKRLITPSE-----APVFVDPHGRGLRALSRQAIDSVLDLACTIVSELSNKK 68
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Db 61 STHAFEGPEKLEIWFYSEKELSPI-----NLDIKPDTWIELNLVHCEVLKSYSSN 113
QY 69 DFDSYVLSSESSLFYPLKIVTKTCTKLLTIPRILE-LABEL-----SMPLA 116
DQ 114 LCDAFLLSSSLFVFPFKIILKTCGTTTILACLDLLFETVKNELLQNEGLKATFQSKNIY 173
QY 117 AVKYSRGTTFPGAQAPHRSPSEVAALNRYFGKLSGNAYVIGDPARPGQKWHVFY- 175
DQ 174 QIFYSRRSPFMPDRQTHVGHNGWQEEVKLLNQYF---NNGKSYIVGN---NTNWHLYVG 225
QY 176 -----ATEYPEQPMVN--LEMCMTGLDKKACVFFKTNADGNTT----- 212
DQ 226 GNGKTKNPVASTTTTTTTPVNDCTLEIIMTQLSLEASQOFTYTRKPGDTAIDSNHDLGH 285
QY 213 -CAKEMTKLSGISEII-----PEMEICD-FDFPCGYSMAIHGSAFSTIH 256
DQ 286 DLQOEILKQTLGNELPFKFKQPTMPGLSSSPKEIHGFAFTPCGFSNINESNYTIIH 345
QY 257 VTPEDGFSYASVEVMGLDATALSYGLVKVLRFCGSPSEFSV 298
DQ 346 VTEPGWSYASFETNMIG----DYKAIVDKCINVPQPGQPMV 383

RESULT 4
US-09-902-540-11867
; Sequence 11867, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11867
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11867

Query Match      4.8%; Score 101.5; DB 4; Length 350;
Best Local Similarity 21.2%; Pred. No. 0.018;
Matches 51; Conservative 28; Mismatches 97; Indels 65; Gaps 9;

QY 171 WH---VFYATEYPEQPMVNLEMCMWTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEII 227
DQ 37 WHVSNVFS-----QPQIDLAAQLTWSGLSRAFFCNSGAENEAALLKLRKVMKDRGTP 91
QY 228 PEMEICDFPEPCGYSMAIHGSAFSTIHVTPEDGFSYASVEVMGLDATALSYGLVKV 287
DQ 92 EREFEVSFD-----SSPHGRTLAIVTATGQAKYQ-KGFEPLPAGFTHPVPGDLEAV 141
QY 288 LRCFGPSEFSVAVTIFGGRG-----HA-----GTWKGAL 316
DQ 142 RKAVGATAAILVEPIQGGGVVMAPIGLVLGRALRCDHEHGLLLLVDEVQTMGRTKGPF 201
QY 317 GAELYDCNNMVQEELP-----GGGLLVYOSFCAAEADAVATSPKSVFHCFDGENVES 367
DQ 202 GF-----MHGIVPDGISVAKALGNLPIGAMLCKEELGASLITPGTHGSTFGNPDVAA 254
QY 368 A 368
DQ 255 A 255

RESULT 5
US-09-010-877-2
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; Sequence 2, Application US/09010877B
; Patent No. 644445
; GENERAL INFORMATION:
; APPLICANT: Walter Reed Army Institute of Research
; APPLICANT: Nikolich, Mikeljon
; APPLICANT: Hoover, David L.
; APPLICANT: Warren, Richard L.
; APPLICANT: Lindler, Luther E.
; APPLICANT: Hadfield, Ted L.
; APPLICANT: Boyle, Stephen M.
; APPLICANT: McQuiston, John R.
; APPLICANT: Schurig, Gerhardt G.
; APPLICANT: Nannalwar Srijangathan
; TITLE OF INVENTION: Live Vaccines Against Brucellosis
; FILE REFERENCE: Army-124
; CURRENT APPLICATION NUMBER: US/09/010,877B
; CURRENT FILING DATE: 1998-01-22
; EARLIER APPLICATION NUMBER: No. 6444445e
; EARLIER FILING DATE: No. 6444445e
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PC-IBM compatible
; SEQ ID NO 2
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Brucella abortus
; US-09-010-877-2

Query Match      4.8%; Score 100.5; DB 4; Length 410;
Best Local Similarity 23.3%; Pred. No. 0.031;
Matches 59; Conservative 33; Mismatches 102; Indels 59; Gaps 13;

QY 69 DPDSYV-LSBSLSFIYPLKIVIKTCGTTKLLTIPRIELABELSMPLAAVKYSRGTFIF 127
Db 179 DAISYAGLPASKVYLAPMEF-----DPTFLDRYSVS-----KVKEPYFLW 219

QY 128 PGAQAPHRFSFEVAALNRYFGLKSGGNAYVIGDPA----RPGQKWHVYATEYPEQPM 184
Db 220 P-TNPNAKHAKHAKAFQALDYGLKGIKTKIVGVSSVRMDPSHRWQAKYEN---KAYV 275

QY 185 VNLEMCWTGLDKKK-----ACVFF-KTNADGNTTCAKEMTKLS-- 221
Db 276 KSVREIVAGLNLKSNVEPAGEVADKEYABELLASACFFWHTLADNGTFAAEEAYMGCP 335

QY 222 GISEIPEMEICDFDFE-PCGYSMNAIH-----GSASFSTIHVTPEDGFSYASVVMGL--- 273
Db 336 TLENDYPMQYISNRFEIPMQY-FNARSVKEMASALKQMEETPIDVGLLPSRETLSHSW 394

QY 274 DATALSYGDLVKR 286
Db 395 EAHASEYWDVIVR 407

RESULT 6
US-07-828-788A-14
; Sequence 14, Application US/07828788A
; Patent No. 5273746
; GENERAL INFORMATION:
; APPLICANT: PAYNE, JEWEL M.
; APPLICANT: HICKLE, LESLIE A.
; TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
; TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID R. SALIWANCHIK
; STREET: 2421 N.W. 41st STREET, SUITE A-1
; CITY: GAINESVILLE
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; Sequence 2, Application US/09010877B
; Patent No. 644445
; GENERAL INFORMATION:
; APPLICANT: Walter Reed Army Institute of Research
; APPLICANT: Nikolich, Mikeljon
; APPLICANT: Hoover, David L.
; APPLICANT: Warren, Richard L.
; APPLICANT: Lindler, Luther E.
; APPLICANT: Hadfield, Ted L.
; APPLICANT: Boyle, Stephen M.
; APPLICANT: McQuiston, John R.
; APPLICANT: Schurig, Gerhardt G.
; APPLICANT: Nannalwar Srijangathan
; TITLE OF INVENTION: Live Vaccines Against Brucellosis
; FILE REFERENCE: Army-124
; CURRENT APPLICATION NUMBER: US/09/010,877B
; CURRENT FILING DATE: 1998-01-22
; EARLIER APPLICATION NUMBER: No. 6444445e
; EARLIER FILING DATE: No. 6444445e
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PC-IBM compatible
; SEQ ID NO 2
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Brucella abortus
; US-09-010-877-2

Query Match      4.8%; Score 100.5; DB 4; Length 410;
Best Local Similarity 23.3%; Pred. No. 0.031;
Matches 59; Conservative 33; Mismatches 102; Indels 59; Gaps 13;

QY 69 DPDSYV-LSBSLSFIYPLKIVIKTCGTTKLLTIPRIELABELSMPLAAVKYSRGTFIF 127
Db 179 DAISYAGLPASKVYLAPMEF-----DPTFLDRYSVS-----KVKEPYFLW 219

QY 128 PGAQAPHRFSFEVAALNRYFGLKSGGNAYVIGDPA----RPGQKWHVYATEYPEQPM 184
Db 220 P-TNPNAKHAKHAKAFQALDYGLKGIKTKIVGVSSVRMDPSHRWQAKYEN---KAYV 275

QY 185 VNLEMCWTGLDKKK-----ACVFF-KTNADGNTTCAKEMTKLS-- 221
Db 276 KSVREIVAGLNLKSNVEPAGEVADKEYABELLASACFFWHTLADNGTFAAEEAYMGCP 335

QY 222 GISEIPEMEICDFDFE-PCGYSMNAIH-----GSASFSTIHVTPEDGFSYASVVMGL--- 273
Db 336 TLENDYPMQYISNRFEIPMQY-FNARSVKEMASALKQMEETPIDVGLLPSRETLSHSW 394

QY 274 DATALSYGDLVKR 286
Db 395 EAHASEYWDVIVR 407

RESULT 6
US-07-828-788A-14
; Sequence 14, Application US/07828788A
; Patent No. 5273746
; GENERAL INFORMATION:
; APPLICANT: PAYNE, JEWEL M.
; APPLICANT: HICKLE, LESLIE A.
; TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
; TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID R. SALIWANCHIK
; STREET: 2421 N.W. 41st STREET, SUITE A-1
; CITY: GAINESVILLE
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/828,788A
; FILING DATE: 19920129
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SALIWANCHIK, DAVID R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA75
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: BACILLUS THURINGIENSIS
; STRAIN: AIZAWAI
; INDIVIDUAL ISOLATE: P8811
; IMMEDIATE SOURCE:
; LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST SICK
; CLONE: 811B
; US-07-828-788A-14

Query Match      4.5%; Score 94; DB 1; Length 1165;
Best Local Similarity 23.4%; Pred. No. 1;
Matches 63; Conservative 30; Mismatches 100; Indels 76; Gaps 14;

QY 35 VDPHGGLALS-----RAQID-SVLDLARCTIVSELNKPDPDSYLVSESSL 80
Db 207 VDTNQGRLRGRFLSDWIVNRRFRQLTISYLD-----IVAFFPNYDIRTPYIQATQ 261

QY 81 FIVPLKIVIKTCGTTKLLTIPRIELABELSMPLAAVKYSRGTFIFGAQPA---PH 135
Db 262 L-----TRVYLDLPFINENLSPAASYP-----TFSNAESAIRSPH 298

QY 136 -----RSFSEEAALNR--YFGG-----LKSGGNAYVIGDP--ARPGQKWHVYATEYPE 181
Db 299 LVDFLNSFTYTDLSARYAYWGHLVNSFRGTGTTTLIRSPLYGREGNTERPVTITASPS 358

QY 182 QPMVNLEMCWTGLDKKKACVFFKTNADGNTTCAKEMTKLSGISEIPEMEICDFDFEPC- 240
Db 359 VFIFRTLSYITGLDLSNPVAGIE-GVEFQNTLSRSYRKSGPIDSFSELPQDASVSPAI 417

QY 241 GYSMNAIH-----GSASFSTIH 256
Db 418 GYSHRLCHATFLERISGPRIAGTVFWSWTH 446

RESULT 7
US-08-356-034-4
; Sequence 4, Application US/08356034
; Patent No. 5691308
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M.
; APPLICANT: Sick, August J.
; TITLE OF INVENTION: No. 5691308el Bacillus thuringiensis Isolate
; TITLE OF INVENTION: Active Against Lepidopteran Pests, and Genes Encoding
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SalIWanchik & SalIWanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606

```

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;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/356,034
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/210,110
;; FILING DATE:
;; FILING DATE: 07/865,168
;; FILING DATE: 09-APR-92
;; APPLICATION NUMBER: 07/451,261
;; FILING DATE: 14-DEC-89
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/371,955
;; FILING DATE: 27-JUN-89
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Saliwanchik, Roman
;; REGISTRATION NUMBER: 21,023
;; REFERENCE/DOCKET NUMBER: MA43.C1.D1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (904)375-8100
;; TELEFAX: (904)372-5800
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1165 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHEetical: YES
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: BACILLUS THURINGIENSIS
;; STRAIN: AIZAWAI
;; INDIVIDUAL ISOLATE: PS81I
;; IMMEDIATE SOURCE:
;; LIBRARY: LAMBDA GEM (TM) - 11 LIBRARY OF AUGUST SICK
;; CLONE: 811B
;; US-08-356-034-4

Query Match 4.5%; Score 94; DB 1; Length 1165;
Best Local Similarity 23.4%; Pred. No. 1;
Matches 63; Conservative 30; Mismatches 100; Indels 76; Gaps 14;

Qy 35 VDPHGRGLRALS-----RAQID-SVLDIARCTIVSELSNKPDSYVLSSESL 80
Db 207 VDTYNOGLRLEGRFLSDWIVNFRRLQTLISVLD-----IVAFFPNYDIRTYPIQTATQ 261

Qy 81 FIYPLKIVIKTCGTTKLLITIPRILE-LABELSMPLAAVKYSGRTFFPGQAQA-----PH 135
Db 262 L-----TREYVLDLPFINENLSPAASYP-----TFSAAESAIIRSPH 298

Qy 136 -----RSFSSEVAALNR--YFGG-----LKSGGNAYVIGDP--ARPGQKWHVFVATEYPE 181
Db 299 LVDFLNSFTIYTSGLARYAWGHLVNSFRIGTTNLRISPLVYRGENTRPTVTITASPS 358

Qy 182 QPMVNLMECTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFDEPC- 240
Db 359 VPIFRLSYITGLDLSNPVAGIE-GVEFQNTISRSIVKSGPIDSPSELPPQDASVSPAI 417

Qy 241 GYSMNIAH-----GSAFSTIH 256
Db 418 GYSHRLCHATFLERISGPIAGTGVFSWTH 446

;; US-08-933-891-4
;; Sequence 4, Application US/08933891
;; Patent No. 6096708
;; GENERAL INFORMATION:
;; APPLICANT: Payne, Jewel M.
;; APPLICANT: Sick, August J.
;; TITLE OF INVENTION: No. 6096708el Bacillus thuringiensis Isolate
;; TITLE OF INVENTION: Active Against Lepidopteran Pests, and Genes Encoding
;; TITLE OF INVENTION: No. 6096708el Lepidopteran-Active Toxins
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Saliwanchik & Saliwanchik
;; STREET: 2421 N.W. 41st Street, Suite A-1
;; CITY: Gainesville
;; STATE: FL
;; COUNTRY: US
;; ZIP: 32606
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/933,891
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/356,034
;; FILING DATE:
;; APPLICATION NUMBER: US/08/210,110
;; FILING DATE:
;; APPLICATION NUMBER: 07/865,168
;; FILING DATE: 09-APR-92
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/451,261
;; FILING DATE: 14-DEC-89
;; APPLICATION NUMBER: 07/371,955
;; FILING DATE: 27-JUN-89
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Saliwanchik, Roman
;; REGISTRATION NUMBER: 21,023
;; REFERENCE/DOCKET NUMBER: MA43.C1.D1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (904)375-8100
;; TELEFAX: (904)372-5800
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1165 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHEtical: YES
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: BACILLUS THURINGIENSIS
;; STRAIN: AIZAWAI
;; INDIVIDUAL ISOLATE: PS81I
;; IMMEDIATE SOURCE:
;; LIBRARY: LAMBDA GEM (TM) - 11 LIBRARY OF AUGUST SICK
;; CLONE: 811B
;; US-08-933-891-4

Query Match 4.5%; Score 94; DB 3; Length 1165;
Best Local Similarity 23.4%; Pred. No. 1;
Matches 63; Conservative 30; Mismatches 100; Indels 76; Gaps 14;

Qy 35 VDPHGRGLRALS-----RAQID-SVLDIARCTIVSELSNKPDSYVLSSESL 80
Db 207 VDTYNOGLRLEGRFLSDWIVNFRRLQTLISVLD-----IVAFFPNYDIRTYPIQTATQ 261

Qy 81 FIYPLKIVIKTCGTTKLLITIPRILE-LABELSMPLAAVKYSGRTFFPGQAQA-----PH 135
Db 262 L-----TREYVLDLPFINENLSPAASYP-----TFSAAESAIIRSPH 298

Qy 136 -----RSFSSEVAALNR--YFGG-----LKSGGNAYVIGDP--ARPGQKWHVFVATEYPE 181
Db 299 LVDFLNSFTIYTSGLARYAWGHLVNSFRIGTTNLRISPLVYRGENTRPTVTITASPS 358

Qy 182 QPMVNLMECTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFDEPC- 240
Db 359 VPIFRLSYITGLDLSNPVAGIE-GVEFQNTISRSIVKSGPIDSPSELPPQDASVSPAI 417

Qy 241 GYSMNIAH-----GSAFSTIH 256
Db 418 GYSHRLCHATFLERISGPIAGTGVFSWTH 446

;; US-08-356-034-4
;; Sequence 4, Application US/08933891
;; Patent No. 6096708
;; GENERAL INFORMATION:
;; APPLICANT: Payne, Jewel M.
;; APPLICANT: Sick, August J.
;; TITLE OF INVENTION: No. 6096708el Bacillus thuringiensis Isolate
;; TITLE OF INVENTION: Active Against Lepidopteran Pests, and Genes Encoding
;; TITLE OF INVENTION: No. 6096708el Lepidopteran-Active Toxins
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Saliwanchik & Saliwanchik
;; STREET: 2421 N.W. 41st Street, Suite A-1
;; CITY: Gainesville
;; STATE: FL
;; COUNTRY: US
;; ZIP: 32606
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/933,891
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/356,034
;; FILING DATE:
;; APPLICATION NUMBER: US/08/210,110
;; FILING DATE:
;; APPLICATION NUMBER: 07/865,168
;; FILING DATE: 09-APR-92
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/451,261
;; FILING DATE: 14-DEC-89
;; APPLICATION NUMBER: 07/371,955
;; FILING DATE: 27-JUN-89
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Saliwanchik, Roman
;; REGISTRATION NUMBER: 21,023
;; REFERENCE/DOCKET NUMBER: MA43.C1.D1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (904)375-8100
;; TELEFAX: (904)372-5800
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1165 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHEtical: YES
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: BACILLUS THURINGIENSIS
;; STRAIN: AIZAWAI
;; INDIVIDUAL ISOLATE: PS81I
;; IMMEDIATE SOURCE:
;; LIBRARY: LAMBDA GEM (TM) - 11 LIBRARY OF AUGUST SICK
;; CLONE: 811B
;; US-08-356-034-4
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Db 262 L-----TREVYLDLPFINENLSPAASYP-----TFSAESAIRSPH 298
Qy 136 -----RSFSEVAALNR--YFGG-----LKSGGNNAVIGDP--ARPGQKWHVFVATEYPE 181
Db 299 LVDFLNSFTIYDLSARYAWGHLVNSFRGTGTTNLRSPLYGREGNTERPVTITASPS 358
Qy 182 QPMVNLEMCMTGLDKKKACVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDFDFEPC- 240
Db 359 VPIFRTLSTYITGLDLSNPVAGIE-GVEFQNTISRSIYRKSGPIDSFSELPQDASVSPAI 417
Qy 241 GYSNNAIH-----GSAFSTIH 256
Db 418 GYSRHLCHATFLERISGPRIAGTVFSWTH 446

RESULT 9

US-09-521-344-4
; Sequence 4, Application US/09521344
; Patent No. 6573240
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M.
; APPLICANT: Sick, August J.
; TITLE OF INVENTION: Lepidopteran Pests, and Genes Encoding No. 6573240e1
; TITLE OF INVENTION: Lepidopteran-Active Toxins
; FILE REFERENCE: MA-43CDP2D2
; CURRENT APPLICATION NUMBER: US/09/521,344
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 08/933,891
; EARLIER FILING DATE: 1997-09-19
; EARLIER APPLICATION NUMBER: US 08/356,034
; EARLIER FILING DATE: 1994-12-14
; EARLIER APPLICATION NUMBER: US 08/210,110
; EARLIER FILING DATE: 1994-03-17
; EARLIER APPLICATION NUMBER: US 07/865,168
; EARLIER FILING DATE: 1992-04-09
; EARLIER APPLICATION NUMBER: US 07/451,261
; EARLIER FILING DATE: 1989-12-14
; EARLIER APPLICATION NUMBER: US 07/371,955
; EARLIER FILING DATE: 1989-06-27
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-521-344-4

Query Match 4.5%; Score 94; DB 4; Length 1165;
Best Local Similarity 23.4%; Pred. No. 1;
Matches 63; Conservative 30; Mismatches 100; Indels 76; Gaps 14;
Qy 35 VDPHGRLRALS-----RAQID-SVLDLARCCTIVSELSNKPDSYVLSSESL 80
Db 207 VDTYNOGLRRLRGRFLSDWIVNRRQLTISVLD-----IVAFPNYDIRTYPIQTATQ 261
Qy 81 FIYPLKIVIKTCGTTKLLLTIPRILE-LABELSNPLAAVKYSGRTFFPGAQPA-----PH 135
Db 262 L-----TREVYLDLPFINENLSPAASYP-----TFSAESAIRSPH 298
Qy 136 -----RSFSEVAALNR--YFGG-----LKSGGNNAVIGDP--ARPGQKWHVFVATEYPE 181
Db 299 LVDFLNSFTIYDLSARYAWGHLVNSFRGTGTTNLRSPLYGREGNTERPVTITASPS 358
Qy 182 QPMVNLEMCMTGLDKKKACVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDFDFEPC- 240
Db 359 VPIFRTLSTYITGLDLSNPVAGIE-GVEFQNTISRSIYRKSGPIDSFSELPQDASVSPAI 417
Qy 241 GYSNNAIH-----GSAFSTIH 256
Db 418 GYSRHLCHATFLERISGPRIAGTVFSWTH 446
Qy 136 -----RSFSEVAALNR--YFGG-----LKSGGNNAVIGDP--ARPGQKWHVFVATEYPE 181
Db 299 LVDFLNSFTIYDLSARYAWGHLVNSFRGTGTTNLRSPLYGREGNTERPVTITASPS 358
Qy 182 QPMVNLEMCMTGLDKKKACVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDFDFEPC- 240
Db 359 VPIFRTLSTYITGLDLSNPVAGIE-GVEFQNTISRSIYRKSGPIDSFSELPQDASVSPAI 417
Qy 241 GYSNNAIH-----GSAFSTIH 256
Db 418 GYSRHLCHATFLERISGPRIAGTVFSWTH 446

RESULT 10

US-09-837-961A-4
; Sequence 4, Application US/09837961A
; Patent No. 6737273
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Sick, August J.
; TITLE OF INVENTION: No. 6737273el Bacillus thuringiensis Isolate Active Against Lepid-
; TITLE OF INVENTION: Pests, and Genes Encoding No. 6737273el Lepidopteran-Active Toxi-
; FILE REFERENCE: MA-43CDP2D3
; CURRENT APPLICATION NUMBER: US/09/837,961A
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/521,344
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 08/933,891
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: US 08/356,034
; PRIOR FILING DATE: 1994-12-14
; PRIOR APPLICATION NUMBER: US 08/210,110
; PRIOR FILING DATE: 1994-03-17
; PRIOR APPLICATION NUMBER: US 07/865,168
; PRIOR FILING DATE: 1992-04-09
; PRIOR APPLICATION NUMBER: US 07/451,261
; PRIOR FILING DATE: 1989-12-14
; PRIOR APPLICATION NUMBER: US 371,955
; PRIOR FILING DATE: 1989-06-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-837-961A-4

Query Match 4.5%; Score 94; DB 4; Length 1165;
Best Local Similarity 23.4%; Pred. No. 1;
Matches 63; Conservative 30; Mismatches 100; Indels 76; Gaps 14;
Qy 35 VDPHGRLRALS-----RAQID-SVLDLARCCTIVSELSNKPDSYVLSSESL 80
Db 207 VDTYNOGLRRLRGRFLSDWIVNRRQLTISVLD-----IVAFPNYDIRTYPIQTATQ 261
Qy 81 FIYPLKIVIKTCGTTKLLLTIPRILE-LABELSNPLAAVKYSGRTFFPGAQPA-----PH 135
Db 262 L-----TREVYLDLPFINENLSPAASYP-----TFSAESAIRSPH 298
Qy 136 -----RSFSEVAALNR--YFGG-----LKSGGNNAVIGDP--ARPGQKWHVFVATEYPE 181
Db 299 LVDFLNSFTIYDLSARYAWGHLVNSFRGTGTTNLRSPLYGREGNTERPVTITASPS 358
Qy 182 QPMVNLEMCMTGLDKKKACVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDFDFEPC- 240
Db 359 VPIFRTLSTYITGLDLSNPVAGIE-GVEFQNTISRSIYRKSGPIDSFSELPQDASVSPAI 417
Qy 241 GYSNNAIH-----GSAFSTIH 256
Db 418 GYSRHLCHATFLERISGPRIAGTVFSWTH 446

RESULT 11

PCT-US92-11337-14
; Sequence 14, Application PC/TUS9211337
; GENERAL INFORMATION:
; APPLICANT: PAYNE, JEWEL M.
; APPLICANT: HICKLE, LESLIE A.
; TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
; TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID R. SALIWANCHIK
; STREET: 2421 N.W. 41st STREET, SUITE A-1
; CITY: GAINESVILLE

; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/11337
; FILING DATE: 19921231
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 97/828,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: SALIWANCHIK, DAVID R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA75
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: BACILLUS THURINGIENSIS
; STRAIN: AIZAWAI
; INDIVIDUAL ISOLATE: P8811
; IMMEDIATE SOURCE:
; LIBRARY: LAMEDAGEM (TM) - 11 LIBRARY OF AUGUST SICK
; CLONE: 811B
; PCT-US92-11337-14

Query Match 4.5%; Score 94; DB 5; Length 1165;
Best Local Similarity 23.4%; Pred. No. 1;
Matches 63; Conservative 30; Mismatches 100; Indels 76; Gaps 14;
QY 35 VDPHGRGLRALS-----RAQID-SVLDLACTIVSELGNKDPDSYVLSSESL 80
Db 207 VDTYNQGLRLEGRFLSDWIVNRRFRQLTISVLD-----IVAFFPNYDIRTYPIQTATQ 261
QY 81 FIYPLKIVIKTCGTTKLLLTIPRIE-LAEELSMPLAAVKYSGRTFFPGAQPA-----PH 135
Db 262 L-----TREYLDLPFINENLSPAASYP-----TFSAAESAIRSPH 298
QY 136 -----RSFSEVAALNR--YFGG-----LKSGGNAYVIGDP--ARPCQKWHVFVATEYPE 181
Db 299 LVDFLNSFTIYDLSARYAYWGHLVNSFRTGTTNLRSPLYRGRENTERPVTITASPS 358
QY 182 QPMVNLEMCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFEPC- 240
Db 359 VPIFRTLVSITGLDNGNPVAGIE-GVEFQNTISRSYRKSGPIDSPSELPPQDASVSPAI 417
QY 241 GYSMNAIH-----GSAFSTIH 256
Db 418 GYSHRLCHATFLERISGPRIAGTVFSWTH 446

RESULT 12
5188960-4
; Patent No. 5188960
; APPLICANT: PAYNE, JEWEL; SICK, AUGUST J.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATE ACTIVE
; AGAINST LEPIDOPTERAN PESTS, AND GENES ENCODING NOVEL
; LEPIDOPTERAN-ACTIVE TOXINS
; NUMBER OF SEQUENCES: 8

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/451,261
; FILING DATE: 14-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 371,955
; FILING DATE: 27-JUN-1989
; SEQ ID NO: 4:
; LENGTH: 1165
; 5188960-4
Query Match 4.5%; Score 94; DB 6; Length 1165;
Best Local Similarity 23.4%; Pred. No. 1;
Matches 63; Conservative 30; Mismatches 100; Indels 76; Gaps 14;
QY 35 VDPHGRGLRALS-----RAQID-SVLDLACTIVSELGNKDPDSYVLSSESL 80
Db 207 VDTYNQGLRLEGRFLSDWIVNRRFRQLTISVLD-----IVAFFPNYDIRTYPIQTATQ 261
QY 81 FIYPLKIVIKTCGTTKLLLTIPRIE-LAEELSMPLAAVKYSGRTFFPGAQPA-----PH 135
Db 262 L-----TREYLDLPFINENLSPAASYP-----TFSAAESAIRSPH 298
QY 136 -----RSFSEVAALNR--YFGG-----LKSGGNAYVIGDP--ARPCQKWHVFVATEYPE 181
Db 299 LVDFLNSFTIYDLSARYAYWGHLVNSFRTGTTNLRSPLYRGRENTERPVTITASPS 358
QY 182 QPMVNLEMCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFEPC- 240
Db 359 VPIFRTLVSITGLDNGNPVAGIE-GVEFQNTISRSYRKSGPIDSPSELPPQDASVSPAI 417
QY 241 GYSMNAIH-----GSAFSTIH 256
Db 418 GYSHRLCHATFLERISGPRIAGTVFSWTH 446

RESULT 13
5188960-4
; Patent No. 5188960
; APPLICANT: PAYNE, JEWEL; SICK, AUGUST J.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATE ACTIVE
; AGAINST LEPIDOPTERAN PESTS, AND GENES ENCODING NOVEL
; LEPIDOPTERAN-ACTIVE TOXINS
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/451,261
; FILING DATE: 14-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 371,955
; FILING DATE: 27-JUN-1989
; SEQ ID NO: 4:
; LENGTH: 1165
; 5188960-4

Query Match 4.5%; Score 94; DB 6; Length 1165;
Best Local Similarity 23.4%; Pred. No. 1;
Matches 63; Conservative 30; Mismatches 100; Indels 76; Gaps 14;
QY 35 VDPHGRGLRALS-----RAQID-SVLDLACTIVSELGNKDPDSYVLSSESL 80
Db 207 VDTYNQGLRLEGRFLSDWIVNRRFRQLTISVLD-----IVAFFPNYDIRTYPIQTATQ 261
QY 81 FIYPLKIVIKTCGTTKLLLTIPRIE-LAEELSMPLAAVKYSGRTFFPGAQPA-----PH 135
Db 262 L-----TREYLDLPFINENLSPAASYP-----TFSAAESAIRSPH 298
QY 136 -----RSFSEVAALNR--YFGG-----LKSGGNAYVIGDP--ARPCQKWHVFVATEYPE 181
Db 299 LVDFLNSFTIYDLSARYAYWGHLVNSFRTGTTNLRSPLYRGRENTERPVTITASPS 358
QY 182 QPMVNLEMCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFEPC- 240
Db 359 VPIFRTLVSITGLDNGNPVAGIE-GVEFQNTISRSYRKSGPIDSPSELPPQDASVSPAI 417

QY 241 GYSNMAIH-----GSAFSTH 256
 Db 418 GYSRLCHATFLERISGRIAGTWSWTH 446

RESULT 14
 US-08-773-368-1
 ; Sequence 1, Application US/08773368
 ; Patent No. 5856130
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Goli, Surya K.
 ; TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED
 ; TITLE OF INVENTION: PROTEIN
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08773,368
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy RJ
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0186 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 270 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; CLONE: 1599164
 ; US-08-773-368-1

Query Match 4.4%; Score 91.5; DB 2; Length 270;
 Best Local Similarity 23.2%; Pred. No. 0.16;
 Matches 63; Conservative 28; Mismatches 108; Indels 73; Gaps 16;
 QY 97 LLITIPRILELA-----EELSMPLAAVKYSGTIFPQAQPAPHRSPSEVAAL 145
 Db 8 LMLLLPLLLLVATTGPGVGTALDEEKKLMVELHNLVRAQ-VSPASDMLHMRWDELAAL 66
 QY 146 NRYFGGL-----KSGGNAYVIGDPA-----PGQKWHVFYATEYPPQPMVNLE--M 189
 Db 67 AKAYARQXRKHNGRGRGENLFAITDEGMDVPLAMEWH-----HEREHYNLSAAT 119
 QY 190 CMTGLDKKAC-----VFFKTNADGNNTCAKEM-TKLSGISIILPEMEICDF----- 235
 Db 120 CSPG-----QMGHYTQVWAKTERIG---CGSHFCEKLGQVEETNIELLVNCPYEPGNVK 172
 QY 236 -----DFEPCGYSMAIH--GSAFSTHVTPEDG--FSYASYEVMGLDATALSYGDLVK 285
 Db 173 GKRPYQEGTFCSPGSGYCKNSLCEPIG-SPEDAQDLPYLVTAPSPFRATEAS-----DS 227
 QY 286 RVLRCFGPSEFSAVITFGGRHAGTWGKALG 317

Db 228 RRMGAEGDPKPSVVSGLNSGPGH--VWGPXLG 257
 RESULT 15
 US-09-199-887-1
 ; Sequence 1, Application US/09199887
 ; Patent No. 6071874
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Goli, Surya K.
 ; TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED
 ; TITLE OF INVENTION: PROTEIN
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09199,887
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/773,368
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy RJ
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0186 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 270 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; CLONE: 1599164
 ; US-09-199-887-1

Query Match 4.4%; Score 91.5; DB 3; Length 270;
 Best Local Similarity 23.2%; Pred. No. 0.16;
 Matches 63; Conservative 28; Mismatches 108; Indels 73; Gaps 16;
 QY 97 LLITIPRILELA-----EELSMPLAAVKYSGTIFPQAQPAPHRSPSEVAAL 145
 Db 8 LMLLLPLLLLVATTGPGVGTALDEEKKLMVELHNLVRAQ-VSPASDMLHMRWDELAAL 66
 QY 146 NRYFGGL-----KSGGNAYVIGDPA-----PGQKWHVFYATEYPPQPMVNLE--M 189
 Db 67 AKAYARQXRKHNGRGRGENLFAITDEGMDVPLAMEWH-----HEREHYNLSAAT 119
 QY 190 CMTGLDKKAC-----VFFKTNADGNNTCAKEM-TKLSGISIILPEMEICDF----- 235
 Db 120 CSPG-----QMGHYTQVWAKTERIG---CGSHFCEKLGQVEETNIELLVNCPYEPGNVK 172
 QY 236 -----DFEPCGYSMAIH--GSAFSTHVTPEDG--FSYASYEVMGLDATALSYGDLVK 285
 Db 173 GKRPYQEGTFCSPGSGYCKNSLCEPIG-SPEDAQDLPYLVTAPSPFRATEAS-----DS 227
 QY 286 RVLRCFGPSEFSAVITFGGRHAGTWGKALG 317

Db 228 RKMGAEGDPKPSVVSLNSGPGH--VMGPXLG 257

Search completed: May 11, 2005, 22:53:54
Job time : 28.4605 secs

GenCore version 5.1.6.
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OM protein - protein search, using sw model

Run on: May 11, 2005, 22:36:02 ; Search time 102.062 Seconds

(without alignments)
1515.788 Million cell updates/sec

Title: US-10-732-923-408

Perfect score: 2097

Sequence: 1 MAVLSAADSPVSAIGPEGY.....LLCWEEDAMEEKAGVLDE 400

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2097	100.0	400	8 ADM48040	Adm48040 Polypepti
2	1687.5	80.5	366	8 ADM48039	Adm48039 Polypepti
3	1019	48.6	237	7 ABM73860	Abm73860 DNA clone
4	933.5	44.5	360	2 AAR75006	Aar75006 Tomato S-
5	933	44.5	363	5 AAU79674	Aau79674 Cucurbita
6	933	44.5	363	7 ABG75228	Abg75228 Plant wit
7	933	44.5	363	8 ADP90956	Adp90956 Figleaf g
8	933	44.5	363	8 ADP38366	Adp38366 Fig leaf
9	881	42.0	366	3 AAG28816	Agg28816 Arabidops
10	806.5	38.5	309	7 ABM73938	Abm73938 DNA clone
11	478.5	22.8	155	7 ABM74096	Abm74096 DNA clone
12	466	22.2	368	8 ADN22644	Adn22644 Bacterial
13	466	22.2	368	8 ADN22643	Adn22643 Bacterial
14	437.5	20.9	369	8 ADN19900	Adn19900 Bacterial
15	424	20.2	348	3 AAB56589	Aab56589 Human pro
16	421.5	20.1	348	4 ABG05997	Abg05997 Novel hum
17	420	20.0	334	5 AAU84313	Aau84313 Protein A
18	420	20.0	334	7 ADE60574	Ad60574 Human Pro
19	420	20.0	334	7 ADD48325	Add48325 Human Pro
20	420	20.0	334	7 ADE60570	Ad60570 Human Pro
21	420	20.0	334	7 ADD48321	Add48321 Human Pro
22	420	20.0	334	8 ADN03708	Adn03708 Antipori
23	420	20.0	334	8 ADQ88208	Adq88208 Human 912
24	419	20.0	333	7 ADE60568	Ad60568 Rat Prote
25	419	20.0	333	7 ADD48323	Add48323 Rat Prote

ALIGNMENTS

RESULT 1

ADM48040
ID ADM48040 standard; protein; 400 AA.

XX AC ADM48040;

XX XX
DT 03-JUN-2004 (first entry)

DE Polypeptide sequence #90 useful in producing transgenic plants.

KW Plant; maize; rice; sorghum; thale cress; soybean; wheat; transgenic;
KW osmotic stress; sugar transport; cell cycle pathway; plant height;
KW carbohydrate transport; crop productivity; plant growth;
KW stress resistance; disease resistance; insect resistance; heat tolerance;
KW nitrogen assimilation; water stress tolerance;
KW photosynthetic carbon fixation; virus resistance; gene therapy.
XX Zea mays.

XX XX
PN US2003233670-A1.

XX XX
PD 18-DEC-2003.

XX XX
PF 04-DEC-2002; 2002US-00310154.

XX XX
PR 04-DEC-2001; 2001US-0337358P.

XX XX
PA (EDGE/) EDGERTON M D.

XX XX
PA (CHOM/) CHOMET P S.

XX XX
PA (LACC/) LACCETTI L B.

XX XX
PI Edgerton MD, Chomet PS, Laccetti LB;

XX XX
DR WPI; 2004-061374/06.

XX XX
DR N-PSDB; ADM47672.

XX XX
PT New polynucleotide, useful for manipulating plant protein quality.
PT Improving plant growth, yield and crop productivity or grain composition
PT or producing plants with improved properties.

XX XX
PS Claim 8; SEQ ID NO 458; 144pp; English.

XX XX
CC The present invention relates to polynucleotide sequences, and the
CC proteins they encode. The sequences are isolated from a variety of
CC organisms such as plants (e.g. maize, rice, sorghum, thale cress,
CC soybean, and wheat), cyanobacteria, bacteria, yeast and other fungi. The
CC polynucleotide and polypeptide sequences of the invention are useful in
CC the production of transgenic plants that have improved properties. Also

CC disclosed are methods of producing fertile transgenic plants, preferably
CC maize, with desired phenotypes. The polynucleotide and polypeptide
CC sequences are useful for improving plants by providing protection against
CC osmotic stress, improving altering sugar transport and/or metabolism,
CC modifying the cell cycle pathway, reducing plant height, modifying
CC carbohydrate transport, improving crop productivity, improving plant
CC growth and stress resistance, improving disease resistance, improving
CC insect resistance, improving cold or heat tolerance, improving nitrogen
CC assimilation, improving stalk strength, improving water stress tolerance,
CC improving photosynthetic carbon fixation, improving biotic and abiotic
CC stress resistance, improving resistance to oxidative stress, providing
CC increased vigour, reducing senescence, and conferring virus resistance.
CC The present sequence represents a polypeptide sequence of the invention.
CC Note: The sequence data for this patent is not provided in the printed
CC specification but is obtained in electronic format from the USPTO website
CC at seqdata.uspto.gov.

XX SQ Sequence 400 AA;

Query Match 100.0%; Score 2097; DB 8; Length 400;
Best Local Similarity 100.0%; Pred. No. 4.1e-206;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAVLSAADASPVSAGFEGYKLEITFSEAPVDPHGRGLRALSRAQIDSVLDLACT 60
DB 1 MAVLSAADASPVSAGFEGYKLEITFSEAPVDPHGRGLRALSRAQIDSVLDLACT 60
QY 61 IVSELSNKFDSYVLSSESLFIYPLKIVITCGTTKLLTIPRIELAEELSMPLAAVKY 120
DB 61 IVSELSNKFDSYVLSSESLFIYPLKIVITCGTTKLLTIPRIELAEELSMPLAAVKY 120
QY 121 SRGTFFPGAQAPHRFSFSEVAALNRYFGLKSGGNAYVIGDAPRGQKWHFYATEYP 180
DB 121 SRGTFFPGAQAPHRFSFSEVAALNRYFGLKSGGNAYVIGDAPRGQKWHFYATEYP 180
QY 181 EQPMVNLKMTGLDKKACVFFKTNADGNTTCAKMTKLSGISEIIPMEICDFDEPC 240
DB 181 EQPMVNLKMTGLDKKACVFFKTNADGNTTCAKMTKLSGISEIIPMEICDFDEPC 240
QY 241 GYSNNAIHGSAFSTHVTVPEDGFSYASYEVMGLDATALSYGDLVKRLRCFGSEFSVAV 300
DB 241 GYSNNAIHGSAFSTHVTVPEDGFSYASYEVMGLDATALSYGDLVKRLRCFGSEFSVAV 300
QY 301 TIFGGRGHAGTWKALGAEVYDCNNMVEQELPGGGLLVYQSFCAAEADAVATSPKSVFHC 360
DB 301 TIFGGRGHAGTWKALGAEVYDCNNMVEQELPGGGLLVYQSFCAAEADAVATSPKSVFHC 360
QY 361 DGENVESAPPPMKDYKLANLLCWEEDADAMEKAGVLDE 400
DB 361 DGENVESAPPPMKDYKLANLLCWEEDADAMEKAGVLDE 400

RESULT 2
ADM48039
ID ADM48039 standard; protein; 366 AA.
XX
AC ADM48039;
XX

03-JUN-2004 (first entry)
XX
XX Polypeptide sequence #89 useful in producing transgenic plants.
DE
XX

XX Plant; maize; rice; sorghum; thale cress; soybean; wheat; transgenic;
KW osmotic stress; sugar transport; cell cycle pathway; plant height;
KW carbohydrate transport; crop productivity; plant growth;
KW stress resistance; disease resistance; insect resistance; heat tolerance;
KW nitrogen assimilation; water stress tolerance;
KW photosynthetic carbon fixation; virus resistance; gene therapy.
XX
OS Zea mays.
XX
XX US2003233670-A1.
PN
XX

PD 18-DEC-2003.
XX
XX 04-DEC-2002; 2002US-00310154.
XX
XX 04-DEC-2001; 2001US-0337358P.
XX
XX (EDGE/) EDGERTON M D.
XX (CHOM/) CHOMET P S.
XX (LACC/) LACCETTI L B.
XX
XX Edgerton MD, Chomet PS, Laccetti LB;
XX
XX WPI; 2004-061374/06.
XX N-PSDB; ADM47671.
XX
XX New polynucleotide, useful for manipulating plant protein quality,
XX improving plant growth, yield and crop productivity or grain composition
XX or producing plants with improved properties.
XX
XX Claim 8; SEQ ID NO 457; 144pp; English.
XX

CC The present invention relates to polynucleotide sequences, and the
CC proteins they encode. The sequences are isolated from a variety of
CC organisms such as plants (e.g. maize, rice, sorghum, thale cress,
CC soybean, and wheat), cyanobacteria, bacteria, yeast and other fungi. The
CC polynucleotide and polypeptide sequences of the invention are useful in
CC the production of transgenic plants that have improved properties. Also
CC disclosed are methods of producing fertile transgenic plants, preferably
CC maize, with desired phenotypes. The polynucleotide and polypeptide
CC sequences are useful for improving plants by providing protection against
CC osmotic stress, improving altering sugar transport and/or metabolism,
CC modifying the cell cycle pathway, reducing plant height, modifying plant
CC carbohydrate transport, improving crop productivity, improving plant
CC growth and stress resistance, improving cold or heat tolerance, improving
CC insect resistance, improving stalk strength, improving water stress tolerance,
CC assimilation, improving photosynthetic carbon fixation, improving biotic and abiotic
CC stress resistance, improving resistance to oxidative stress, providing
CC increased vigour, reducing senescence, and conferring virus resistance.
CC The present sequence represents a polypeptide sequence of the invention.
CC Note: The sequence data for this patent is not provided in the printed
CC specification but is obtained in electronic format from the USPTO website
CC at seqdata.uspto.gov.

XX SQ Sequence 366 AA;

Query Match 80.5%; Score 1687.5; DB 8; Length 366;
Best Local Similarity 85.0%; Pred. No. 4.4e-164;
Matches 328; Conservative 7; Mismatches 20; Indels 31; Gaps 2;
QY 1 MAVLSAADASPVSAGFEGYKLEITFSEAPVDPHGRGLRALSRAQIDSVLDLACT 60
DB 1 MAVLSAADASPVSAGFEGYKLEITFSEAPVDPHGRGLRALSRAQIDSVLDLACT 60
QY 61 IVSELSNKFDSYVLSSESLFIYPLKIVITCGTTKLLTIPRIELAEELSMPLAAVKY 120
DB 59 -----KIVITCGTTKLLTIPRIELAEELSMPLAAVKY 93
QY 121 SRGTFFPGAQAPHRFSFSEVAALNRYFGLKSGGNAYVIGDAPRGQKWHFYATEYP 180
DB 94 SRGTFFPGAQAPHRFSFSEVAALNRYFGLKSGGNAYVIGDAPRGQKWHFYATEYP 153
QY 181 EQPMVNLKMTGLDKKACVFFKTNADGNTTCAKMTKLSGISEIIPMEICDFDEPC 240
DB 154 EQPMVNLKMTGLDKKACVFFKTNADGNTTCAKMTKLSGISEIIPMEICDFDEPC 213
QY 241 GYSNNAIHGSAFSTHVTVPEDGFSYASYEVMGLDATALSYGDLVKRLRCFGSEFSVAV 300
DB 214 GYSNNAIHGSAFSTHVTVPEDGFSYASYEVMGLDATALSYGDLVKRLRCFGSEFSVAV 273
QY 301 TIFGGRGHAGTWKALGAEVYDCNNMVEQELPGGGLLVYQSFCAAEADAVATSPKSVFHC 360
DB 274 TIFGGRGHAGTWKALGAEVYDCNNMVEQELPGGGLLVYQSFCAAEADAVATSPKSVLRCF 333


```

Db 241 EGAAVSTIHITPEDGFTYASFESGVYDPKTNELPLVERVLACFEPAPERSIAL----- 293
Qy 308 HAGTWGKAL-----GAEVDCNNWVEQLPGGGLLYVQSFCAEDAVATSPKSVFHCFD 361
Db 294 HADVATKLLSHVCSVDVKGYSLAWSPEEFGKGSIVYQKF--TRTPCYCESPKSVLKG-- 349
Qy 362 GENVESAPPPMKDYKLANLLCWEEEDAMEEKAG 396
Db 350 -----CWKE-----EKEG 358

RESULT 5
AAU79674
ID AAU79674 standard; protein; 363 AA.
XX AC AAU79674;
XX DT 15-JUL-2002 (first entry)
XX DE Cucurbita ficifolia S-adenosylmethionine decarboxylase (SAMDC).
XX KW Plant; polyamine metabolism-related enzyme; environmental stress;
XX KW vegetable; fruit; flower; food; agriculture; horticulture;
XX KW temperature stress; drought; improved growth; SAMDC;
XX KW S-adenosylmethionine decarboxylase; enzyme.
XX OS Cucurbita ficifolia.
XX PN WO200223974-A1.
XX PD 28-MAR-2002.
XX PF 31-AUG-2001; 2001WO-JP007521.
XX PR 20-SEP-2000; 2000JP-00285423.
XX PR 08-FEB-2001; 2001JP-00032627.
XX PA (TOYO-) TOYOBO RES CENT CO LTD.
XX PI Kasukabe Y, Ihara I, Tachibana S;
XX WPI; 2002-329978/36.
XX N-PSDB; ABK48732.

Plant for selecting new breeds of e.g. vegetables, fruits and flowers for
food and decoration, comprises improved tolerance to environmental
stresses transferred with a plant-originated polyamine metabolism-
relating enzyme gene.

Disclosure; Page 85-88; 108pp; Japanese.

The present invention relates to the isolation of a plant derived
polyamine metabolism-related enzyme gene. Also described is a plant
having improved tolerance to environmental stresses that can stably
sustain an exogenous polyamine metabolism-related enzyme gene by
regulation of a promoter functioning in such plant, as compared to plants
free from the exogenous gene, or its descendants. The plant is useful in
selecting new breeds of e.g. vegetables, fruits and flowers for food and
decoration, particularly applicable in agriculture and horticulture. The
transgenic plants have improved tolerance to various environmental
stresses e.g. temperature and drought, and also have excellent growth.
The present sequence represents Cucurbita ficifolia S-adenosylmethionine
decarboxylase (SAMDC)

Sequence 363 AA;
Query Match 44.5%; Score 933; DB 5; Length 363;
Best Local Similarity 50.9%; Pred. No. 1.5e-86;
Matches 201; Conservative 53; Mismatches 95; Indels 46; Gaps 9;

Qy 11 PVSAGFEGYKRLITFSAPVFDVPHGRGLRALSQAQIDSVLDLACTIVSELNSKDF 70
Db 4 PTAIGFEGYKRLVSVFPEFGIFADPRGNGLRALSQAQIDILTLAECTIVDSLNDYL 63

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```

Qy 71 DSVLSESLFIYPLKIVIKTCGTTKLLLTIPRILELAELSMPAAVKYSGTFFRGA 130
Db 64 DSVLSESLFVVPYPIKTCGTTKLLSLPALIKLADSLNVKSVRTRGSFIFPGA 123
Qy 131 QPAPHRFSFSEVAALNRYFGGLKSGGNVYIGDPAIPGQKWHVYAT-----EYEQPMVN 186
Db 124 QSPFHRFSFSEVAALNRYFGGLKSGGNVYIGDPAIPGQKWHVYAT-----EYEQPMVN 182
Qy 187 LEMCMTGLDKKACVFFKTNADONTTCAKEMTKLSGISEIIPMEICDFDFPCGYSMNA 246
Db 183 LEMCMTGLDKKACVFFKTNADONTTCAKEMTKLSGISEIIPMEICDFDFPCGYSMNA 238
Qy 247 IHGSAFSTHVTPEDEGFSYASVEMGLDATALSYGLDKVLRVRCFQSPSESVAVTIFGGR 306
Db 239 IEGDABSTHVTPEDEGFSYASVEMGLDATALSYGLDKVLRVRCFQSPSESVAVTIFGGR 292
Qy 307 GHAGTWGK-----ALGAEVYDCNNWVEQLPGGGLLYVQSFCAEDAVATSPKSVFHC 360
Db 293 -HSDVVGEDLKDLLCLDLKGYEGEKSCMLGENGSVIYQSFKNRGD-YASSPRSL--- 347
Qy 361 DGENVESAPPPMKDYKLANLLCW-EEEDAMEEK 394
Db 348 -----MK-----CCWREDEADEVEK 363

RESULT 6
ABG75228
ID ABG75228 standard; protein; 363 AA.
XX AC ABG75228;
XX DT 12-FEB-2004 (first entry)
XX DE Plant with improved organogenesis related protein SEQ ID NO: 4.
XX KW Organogenesis; polyamine metabolism-associated gene; transgenic;
XX KW drug production; biodegradable plastic; enzyme production;
XX KW vaccine production; promoter; plant; callus.
XX OS Cucurbita ficifolia.
XX PN WO2003084314-A1.
XX PD 16-OCT-2003.
XX PF 08-APR-2003; 2003WO-JP004427.
XX PR 08-APR-2002; 2002JP-00105583.
XX PA (TOYO-) TOYOBO RES CENT CO LTD.
XX PI Kasukabe Y, Ihara I, Tachibana S, Matsui K, Mizutani M;
XX WPI; 2003-833547/77.
XX N-PSDB; ACF04931.

Construction of plants with improved organogenesis of e.g. stem, leaf,
flower, fruit or seed for retaining plant-originated polyamine metabolism
-associated gene, applicable in producing useful substances including
drugs.

Claim 7; Page 70-72; Opp; Japanese.

The present invention relates to plants and their offspring which stably
retain 1 or more nucleic acid sequences for regulating polyamine dose
under the control of a promoter functionally in the plant and have at
least an improved organogenesis as compared with plants without such
nucleic acid sequences. The constructed plants are applicable in
producing useful substances including drugs, biodegradable plastics,
CC vaccines and enzymes. Such method is particularly applicable in
CC agriculture and horticulture. The present sequence is a protein shown in
CC the exemplification of the invention

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PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 18-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
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PR 05-AUG-1999; 99US-0147192P.
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PR 06-AUG-1999; 99US-0147303P.
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PR 09-AUG-1999; 99US-0147935P.
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PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
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PR 27-AUG-1999; 99US-0151065P.
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PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
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PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.

PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
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PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
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PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161405P.
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PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 42.0%; Score 881; DB 3; Length 366;
Best Local Similarity 50.7%; Pred. No. 3 4e-81;
Matches 185; Conservative 49; Mismatches 95; Indels 36; Gaps 8;

QY 12 VSAIGPEGYKRLKLEITFSEAPVDPHGRGLRALSAQIDSVLDLACTIVSELNKPFD 71
Db 3 LSAIGPEGYKRLKLEITFSEAPVDPHGRGLRALSAQIDSVLDLACTIVSELNKPFD 62
QY 72 SYVLSESLFIYPLKIVIKTCGTTKLLLTIPRILELAELSMPAAVKYSGTFFPQAQ 131
Db 63 SYVLSESLFIYPLKIVIKTCGTTKLLLTIPRILELAELSMPAAVKYSGTFFPQAQ 122
QY 132 PAPHRSFSEVAALNRYFGGLKSGGNAYVIGDPAKQKWHVYATYEPQPMVN---L 187
Db 123 PPHRSFSEVSVLDGHFTQLGLNSVAYLMGNDET-KKWHVYAAQAQSSNCNNVYTL 181
QY 188 EMCMTGLDKKACVFPKTNADGNTTCAKEMTKLSGISEIPEMEICDFPFCGYSNNAI 247
Db 182 EMCMTGLDKKAAVFKDEADKTGS---MTDNGIRKILPKSEICDFPFCGYSNNAI 237
QY 248 HGSASFTHVTPEDEGFSYASYEVMGLDATALSYGDLVKVLRFCGFSERSVATIFGGRG 307
Db 238 EGDASTHVTPEDEGFSYASYEVMGLDATALSYGDLVKVLRFCGFSERSVATIFGGRG 290
QY 308 HAGTWGKALGAEV-----YDCNNMVEQEL-PGGGLLVYQSF-----CAEDAVATSPK 354
Db 291 HSSVGANSYKPEITVDLEDYGCRTFESLGESGTVMTQTFEKLKYCG-----SPR 343
QY 355 SVFPHC 359
Db 344 STLKC 348

RESULT 10
ABM73938
ID ABM73938 standard; protein; 309 AA.

```

XX AC ABW73938;
XX DT 17-OCT-2003 (first entry)
XX DE DNA clone originating in barley containing SNP sequence #348.
XX KW Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.
XX OS Hordeum vulgare.
XX PN WO2003057877-A1.
XX PD 17-JUL-2003.
XX PF 16-DEC-2002; 2002WO-IB005403.
XX PR 20-DEC-2001; 2001JP-00387059.
XX PR 20-DEC-2001; 2001JP-00387131.
XX PR 20-DEC-2001; 2001JP-00403299.
XX PR 20-DEC-2001; 2001JP-00403300.
XX PR 27-SEP-2002; 2002JP-00327515.
XX PA (UYNI-) UNIV JAPAN OKAYAMA.
XX PI Sato K, Takeda K, Kohara Y;
XX DR WPI; 2003-587127/55.
XX PS Single nucleotide polymorphism sites in barley varieties and DNA
XX PT sequences containing them for analysis and identification of barley
XX PT varieties and production of barley transformants with desired
XX PT characteristics.
XX PS Disclosure; SEQ ID XX; 284pp; Japanese.
XX CC The present invention relates to oligonucleotide clones originating in
XX CC barley (Hordeum vulgare) which contain single nucleotide polymorphisms
XX CC (SNP). The oligonucleotides may be used for analysis of SNPs among barley
XX CC varieties, identification of particular varieties and genotype-phenotype
XX CC analysis, isolation of specific genes and creation of new varieties by
XX CC transformation of barley varieties with them and production of new barley
XX CC varieties with desired properties. The present sequence represents an
XX CC oligonucleotide clone sequence featured in the specification. The
XX CC sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published-pct-sequences
XX SQ Sequence 309 AA;
XX
Query Match 39.5%; Score 806.5; DB 7; Length 309;
Best Local Similarity 64.8%; Pred. No. 1.2e-73;
Matches 171; Conservative 13; Mismatches 47; Indels 33; Gaps 4;

QY 68 KDFSVYLVSSSLFIYPLKIVIKTCGTTKLLLTIPRILELAELSMPLAAVKYSRGTFIF 127
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
31 RFDYSYLVSSSLFIYQKIVIKTCGTTMLLLTIPRILELAELCMPLAAVKYSRGMFIF 90
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 128 PGAQAPHRFSBEVALNRYFGLKSGGNAYVIGDPAPQKQWVHYATEYPEQPMVNL 187
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
91 PGAQAPHRFSBEVDVLYNYFGLKSGGNAYVIGDPAPQKQWVHYATEYPEQPMVTL 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 188 EMCWTGLDKKACVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDFPE----- 238
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
151 EMCWTGLDKKASVFFKTSADGHVCAKEMTKLSGISIIPEMEVCDFPEALRLHLHERH 210
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 239 -----PCGYSNNAIHGSAFTIHTVTPEDGFSYASYEVWGLDATALSYGLVKVRLC 290
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
211 QRCLLHHPCDPRTASATAMRSRAWTPPP-WSTATSRGSGCASALQ-----SS 260
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 291 FGPSEFSVAVTIFGGRGHAGTWGK 314
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
261 LWRSPSSVAA-----GHAATWGO 278
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 11
ABW74096
ID ABW74096 standard; protein; 155 AA.
XX AC ABW74096;
XX DT 17-OCT-2003 (first entry)
XX DE DNA clone originating in barley containing SNP sequence #506.
XX KW Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.
XX OS Hordeum vulgare.
XX PN WO2003057877-A1.
XX PD 17-JUL-2003.
XX PF 16-DEC-2002; 2002WO-IB005403.
XX PR 20-DEC-2001; 2001JP-00387059.
XX PR 20-DEC-2001; 2001JP-00387131.
XX PR 20-DEC-2001; 2001JP-00403299.
XX PR 20-DEC-2001; 2001JP-00403300.
XX PR 27-SEP-2002; 2002JP-00327515.
XX PA (UYNI-) UNIV JAPAN OKAYAMA.
XX PI Sato K, Takeda K, Kohara Y;
XX DR WPI; 2003-587127/55.
XX PS Single nucleotide polymorphism sites in barley varieties and DNA
XX PT sequences containing them for analysis and identification of barley
XX PT varieties and production of barley transformants with desired
XX PT characteristics.
XX PS Disclosure; SEQ ID XX; 284pp; Japanese.
XX CC The present invention relates to oligonucleotide clones originating in
XX CC barley (Hordeum vulgare) which contain single nucleotide polymorphisms
XX CC (SNP). The oligonucleotides may be used for analysis of SNPs among barley
XX CC varieties, identification of particular varieties and genotype-phenotype
XX CC analysis, isolation of specific genes and creation of new varieties by
XX CC transformation of barley varieties with them and production of new barley
XX CC varieties with desired properties. The present sequence represents an
XX CC oligonucleotide clone sequence featured in the specification. The
XX CC sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published-pct-sequences
XX SQ Sequence 155 AA;
XX
Query Match 22.8%; Score 478.5; DB 7; Length 155;
Best Local Similarity 64.2%; Pred. No. 2.1e-40;
Matches 97; Conservative 15; Mismatches 30; Indels 9; Gaps 2;

QY 244 MNAIHGSAFTIHTVTPEDGFSYASYEVWGLDATALSYGLVKVRLCFGPSEFSVAVTIF 303
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MNAIHGSAFTIHTVTPEDGFSYGYEVWGLDPASMAVGLVKVRLSFGSEFSVAVTIF 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 304 GGRGHAGTWGKALGAEVYDCNNVVEQELPGGGLLVYQSFCAAEADAVATSPKVPFHCDFGE 363
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 GCFSLAGTWGERLVNGVYDSTNVVQELPGGGLIYQSFATAAGDSGSPRSVLCVVDG 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 364 NVESAPPPMKDYKLANLLCWEEADAMEEK 394
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 NLOQAS-----KVDAFLCWED--DAAQEK 142
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12

```


Db 234 NLGGHILGSYVADESGVRDLCTSDKKAVALDAFQPEPIGFSNNMIYKORIATIHVTPQE 293
QY 262 GFSYASYEVNGLDATALSYG----DLVKRLRCFGPSEFSVAVTIFGGRGHAGTWGKALG 317
Db 294 HCSYASFET---NVSQFQGRSISEITKVTKFGANKF--CLTLFQAKG--ASQEKHFS 346
QY 318 AEV-----YDCNNMVRQELPG 333
Db 347 AKLKSPSSYKREBFIVYDFPG 367

RESULT 15
AAB56589
ID AAB56589 standard; protein; 348 AA.
XX AC AAB56589;
XX DT 13-MAR-2001 (first entry)
XX DE Human prostate cancer antigen protein sequence SEQ ID NO:1167.
XX KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
KW vulnery; gastrointestinal; nephrotropic; antiinfective; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease.
XX OS Homo sapiens.
XX PN WO200055174-A1.
XX PD 21-SEP-2000.
XX PF 08-MAR-2000; 2000WO-US005988.
XX PR 12-MAR-1999; 99US-0124270P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (ROSE/) ROSEN C A.
XX PI Rosen CA, Ruben SM;
XX WPI; 2000-587513/55.
XX DR N-PSDB; AAF15792.
XX PT Prostate cancer associated gene sequences, referred to as prostate cancer
PT antigens, useful for treatment, prevention, and diagnosis of disorders
PT such as prostate cancer.
XX PS Claim 11; Page 1573-1575; 2338pp; English.
XX CC AAF15566 to AAF16505 encode the human prostate cancer associated
CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
CC The prostate cancer antigens can have neuroprotective, cytostatic,
CC cardioactive, immunomodulatory, muscular, vulnery, gastrointestinal,
CC nephrotropic, antiinfective, gynaecological and antibacterial activities,
CC and can be used in gene therapy. The prostate cancer antigen
CC polynucleotides may be used for detection of prostate cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The prostate cancer antigens may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
CC AAB57303 represent sequences used in the exemplification of the present
CC invention
XX SQ Sequence 348 AA;

Query Match 20.2%; Score 424; DB 3; Length 348;
Best Local Similarity 36.9%; Pred. No. 2.9e-34;
Matches 109; Conservative 48; Mismatches 114; Indels 24; Gaps 9;

QY 17 FEGYEKRLBITTSEAPVFDVPHGRGRALRSRAQIDSVLDLARCTIVSELSNKDFDSYVLS 76
Db 21 FEGETKLELVWFESRQOPDANQSGDRLTIPRSEWDILLKDVQCSIISVTKTDRQEAAYLS 80
QY 77 ESSLFYIPLKIVIKTCGTTKLLLTIPRILELAELS--MPLAAVKYSRGTFFPGQAPAP 134
Db 81 ESSMFVSKRRFILKTCGTTLLKALVPLKLDYSGFDSIQSFFYSRKNFMKPSHQGY 140
QY 135 HRSFSEVAALNRYFGGLKSGGNAYVIGDPARPGQKWHVFAYEYPE-----OPMVNLEM 189
Db 141 HRNFQEEIEFLNAIF-----PNGAAYCMG---RNSDCWLYTLDFPESRVISQPDQTL 193
QY 190 CMTGLDKKAKCVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFPCGYSMAIHG 249
Db 194 LMSELDPAVMDQFYM--KQGV--AKDVTRESGIRDLIPGSVIDATMFMPCGYSMNGMKS 249
QY 250 -SAFSTIHVTPEDGFSYASYEVNGLDATALSYCDLVKRLRCFGPSEFSVAVTIF 303
Db 250 DGTYTHTHTPEPESYVSFET---NLSQTSYDDLLIRKVVVEFKPGK--VTTLF 299

Search completed: May 11, 2005, 22:47:51
Job time : 103.062 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 11, 2005, 22:38:57 ; Search time 86.9416 Seconds
(without alignments)
2167.492 Million cell updates/sec

Title: US-10-732-923-407

Perfect score: 1914

Sequence: 1 MAVLSAAGAPPASAIAGFEY.....NLVLCLEEXDAIERKGVLDSE 368

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1726	90.2	400	1	DCAM_MAIZE	O24575 zea mays (m
2	1538	80.4	398	1	DCAM_ORYZA	O24215 oryza sativ
3	1538	80.4	398	2	O7X783	O7X783 oryza sativ
4	1472.5	76.9	393	1	DCAM_HORCH	O42829 hordeum chi
5	1460	76.3	392	2	O9ZFU1	O9ZFU1 triticum ae
6	1458	76.2	395	2	O6K9B8	O6K9B8 oryza sativ
7	1458	76.2	395	2	O9SC67	O9SC67 oryza sativ
8	1244	65.0	392	2	O6F4N6	O6F4N6 oryza sativ
9	1187.5	62.0	370	2	O84LA2	O84LA2 narcissus p
10	1160	60.6	369	2	O944U3	O944U3 dendrobium
11	1134.5	59.3	319	2	O7XZQ9	O7XZQ9 oryza sativ
12	858	44.8	358	2	O9F8M2	O9F8M2 vitis vinif
13	854.5	44.6	357	1	DCAM_CATRO	O42679 catharanthu
14	851	44.5	353	1	DCAM_VICFA	O9M488 vicia faba
15	841	43.9	363	1	DCAM_SPIOL	P46255 spinacia ol
16	836	43.7	362	1	DCAM_IPONI	O96471 ipomoea nil
17	834.5	43.6	361	1	DCAM_NICSY	O80402 nicotiana s
18	834.5	43.6	361	1	DCAM_TOBAC	O04009 nicotiana t
19	834	43.6	353	1	DCAM_PEA	O43820 pisum sativ
20	833.5	43.5	349	2	O9L5U6	O9L5U6 arabidopsis
21	833.5	43.5	358	2	O852S9	O852S9 malus domes
22	832.5	43.5	374	2	O852S8	O852S8 malus domes
23	830	43.4	362	1	DCAM_DATST	O96555 datura stra
24	830	43.4	362	1	DCAM_IPOBA	O9M6K1 ipomoea bat
25	826.5	43.2	354	2	O8W3Y2	O8W3Y2 phaseolus l
26	825.5	43.1	381	1	DCAL_DIACA	O39676 dianthus ca
27	824.5	43.1	377	1	DCA2_DIACA	O39677 dianthus ca
28	821.5	42.9	361	2	O8LKJ7	O8LKJ7 x citrofor
29	812.5	42.5	360	1	DCAM_SOLTU	O04694 solanum tub
30	809	42.3	355	2	O8S3F8	O8S3F8 glycine max
31	798.5	41.7	361	2	O6RUQ3	O6RUQ3 daucus caro

32 792.5 41.4 361 1 DCAM_DAUCA
33 771.5 40.3 366 1 DCAL_ARATH
34 769.5 40.2 366 2 O6QJ69
35 766.5 40.0 366 2 O94Q05
36 763.5 39.9 361 1 DCAM_HELAN
37 763 39.9 367 1 DCA3_BRAJU
38 757 39.6 362 1 DCA2_ARATH
39 753 39.3 369 2 O6SZS4
40 751 39.2 369 1 DCA2_BRAJU
41 718.5 37.5 279 2 O76KV7
42 706.5 36.9 368 1 DCAL_BRAJU
43 668.5 34.9 309 2 O6KC47
44 609.5 31.8 169 2 O9SC65
45 574.5 30.0 228 2 Q8VX33

ALIGNMENTS

RESULT 1

ID DCAM_MAIZE STANDARD; PRT; 400 AA.

AC O24575; 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)

DE (SambC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-

DE adenosylmethionine decarboxylase beta chain].

GN Name=SAMDC;

OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC PACCAD clade; Panicoideae; Andropogoneae; Zea.

OX NCBI_TaxID=4577;

RP [1]

RN SEQUENCE FROM N.A.

RA Michael A.J.;

RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S-deoxy-5-

adenosyl) (3-aminopropyl)-methylsulfonium salt + CO(2).

CC -1- COFACTOR: Pyruvoyl group (By similarity).

CC -1- PATHWAY: Decarboxylation of S-adenosylmethionine provides the

aminopropyl moiety required for spermidine and spermine

biosynthesis from putrescine.

CC -1- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation -

the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial

entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

or send an email to license@isb-sib.ch).

CC EMBL; Y07767; CAA69075.1; -

DR PIR; T03947; T03947.

DR HSP; P17707; IJEN.

DR InterPro; IPR001985; SAM decarbox.

DR Pfam; PF01536; SAM decarbox; 1.

DR ProDom; PD002379; SAM decarbox; 1.

DR TIGRfams; TIGR00535; SAM.DCase; 1.

DR PROSITE; PS01336; ADOMETDC; 1.

KW Decarboxylase; Lyase; Pyruvate; Spermidine biosynthesis; Zymogen.

CHAIN 1 77 S-adenosylmethionine decarboxylase beta

chain (By similarity).

CHAIN 78 400 S-adenosylmethionine decarboxylase alpha

chain (By similarity).

FT SITE 77 78 Cleavage (nonhydrolytic) (By similarity).

FT MOD_RES 78 78 Pyruvic acid (Ser) (By similarity).

FT ACT_SITE 18 18 By similarity.

FT ACT_SITE 21 21 By similarity.

FT ACT_SITE 92 92 By similarity.

FT ACT_SITE 92 92 By similarity.

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SQ SEQUENCE 400 AA; 43515 MW; 1B2445775F55714A CRC64;
Query Match 90.2%; Score 1726; DB 1; Length 400;
Best Local Similarity 84.5%; Pred. No. 5.8e-136;
Matches 338; Conservative 8; Mismatches 22; Indels 32; Gaps 3;
QY 1 MAVLSAAGAPPASAIAGFEGYKLEITTFSEAPVFDPHGSLRALSRQSDSVLDLAR-- 58
DB 1 MAVLSAADASPVSAIGFEGYKLEITTFSEAPVFDPHGSLRALSRQSDSVLDLARCT 60
QY 59 -----KIVIKTCGTTKLLTIPRIELAEBSLPLAAVKY 93
DB 61 IVSELSNKKDFDSYVLSSESLFIYPLKIVIKTCGTTKLLTIPRIELAEBSLPLAAVKY 120
QY 94 SRGTFTFPGAQAPAPHSFSEAVLNRYFGGLSGGNVAVIGDAAPGQKWHIYYATEYP 153
DB 121 SRGTFTFPGAQAPAPHSFSEAVLNRYFGGLSGGNVAVIGDAAPGQKWHIYYATEYP 180
QY 154 EQPMVNLKMTGLDTPKASVFFKTNADGNNTTCAKEMTKLSGISEIIPEMEICDFDFEPC 213
DB 181 EQPMVNLKMTGLDTPKASVFFKTNADGNNTTCAKEMTKLSGISEIIPEMEICDFDFEPC 240
QY 214 GYSMNAIHGSAFSTIHTVTPEDGFSYASYEVMGLDATALSYGDLVKRVLRCFGSSEFSVAV 273
DB 241 GYSMNAIHGSAFSTIHTVTPEDGFSYASYEVMGLDATALSYGDLVKRVLRCFGSSEFSVAV 300
QY 274 TIFGGRGAGTGWKELGAAYDCNNVVEQLPGLGGILIIYQSFCAAED--AVASSPKSVLR 331
DB 301 TIFGGRGAGTGWKELGAAYDCNNVVEQLPGLGGILIIYQSFCAAED--AVASSPKSVLR 360
QY 332 CDFGE---NAAPPKACKLANLVCLREXDAIEKDGVLDE 368
DB 361 CFEAENWVPAP-VKESKLGKLNLLPWGE-DALENDGVFDE 398
RESULT 3
Q7XT83 PRELIMINARY; PRT; 398 AA.
AC Q7XT83; Q7XUL0;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE OSJNBa0029H02.2 protein (OSJNBa0067K08.23 protein).
GN Names=OSJNBa0029H02.2; Synonyms=OSJNBa0067K08.23;
OS Oryza sativa (japonica cultivar-group).
SQ SEQUENCE 400 AA; 43515 MW; 1B2445775F55714A CRC64;
Query Match 90.2%; Score 1726; DB 1; Length 400;
Best Local Similarity 84.5%; Pred. No. 5.8e-136;
Matches 338; Conservative 8; Mismatches 22; Indels 32; Gaps 3;
QY 1 MAVLSAAGAPPASAIAGFEGYKLEITTFSEAPVFDPHGSLRALSRQSDSVLDLAR-- 58
DB 1 MAVLSAADASPVSAIGFEGYKLEITTFSEAPVFDPHGSLRALSRQSDSVLDLARCT 60
QY 59 -----KIVIKTCGTTKLLTIPRIELAEBSLPLAAVKY 93
DB 61 IVSELSNKKDFDSYVLSSESLFIYPLKIVIKTCGTTKLLTIPRIELAEBSLPLAAVKY 120
QY 94 SRGTFTFPGAQAPAPHSFSEAVLNRYFGGLSGGNVAVIGDAAPGQKWHIYYATEYP 153
DB 121 SRGTFTFPGAQAPAPHSFSEAVLNRYFGGLSGGNVAVIGDAAPGQKWHIYYATEYP 180
QY 154 EQPMVNLKMTGLDTPKASVFFKTNADGNNTTCAKEMTKLSGISEIIPEMEICDFDFEPC 213
DB 181 EQPMVNLKMTGLDTPKASVFFKTNADGNNTTCAKEMTKLSGISEIIPEMEICDFDFEPC 240
QY 214 GYSMNAIHGSAFSTIHTVTPEDGFSYASYEVMGLDATALSYGDLVKRVLRCFGSSEFSVAV 273
DB 241 GYSMNAIHGSAFSTIHTVTPEDGFSYASYEVMGLDATALSYGDLVKRVLRCFGSSEFSVAV 300
QY 274 TIFGGRGAGTGWKELGAAYDCNNVVEQLPGLGGILIIYQSFCAAEDAVASSPKSVLR 331
DB 301 TIFGGRGAGTGWKELGAAYDCNNVVEQLPGLGGILIIYQSFCAAEDAVASSPKSVLR 360
QY 332 CDFGE---NAAPPKACKLANLVCLREXDAIEKDGVLDE 368
DB 361 CFEAENWVPAP-VKESKLGKLNLLPWGE-DALENDGVFDE 398
RESULT 2
DCAM_ORYSA STANDARD; PRT; 398 AA.
AC 024215; 081269;
DT 15-DEC-1998 (Rel. 37, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
DE (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain].
GN Name=SAMDC;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoideae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica / Nipponbare;
RX MEDLINE=2106609; PubMed=11139406; DOI=10.1042/0264-6021:3530403;
RA Franceschetti M., Hanfrey C., Scaramagli S., Torrigiani P., Bagni N., Michael A.J.;
RA "Characterization of monocot and dicot plant S-adenosyl-L-methionine decarboxylase gene families including identification in the mRNA of a highly conserved pair of upstream overlapping open reading frames.";
RL Biochem. J. 353:403-409(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Li Z.Y., Chen S.Y.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -I- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S-deoxy-5-adenosyl) (3-aminopropyl)-methylsulfonium salt + CO(2).
CC -I- COFACTOR: Pyruvoyl group.
CC -I- PATHWAY: Decarboxylation of S-adenosylmethionine provides the aminopropyl moiety required for spermidine and spermine biosynthesis from putrescine.
CC -I- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.
-----
```

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=12447439; DOI=10.1038/nature01183;
 RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
 RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
 RA Wang Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
 RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
 RA Wu M., Zhang R., Zhou B., Chen Z., Wang R., Wang R., Yin H.,
 RA Cai Z., Ren S., Lu G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
 RA Chen J., Chang H., Shao X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
 RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
 RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
 RA Han B.;
 RT "Sequence and analysis of rice chromosome 4.";
 RL Nature 420:316-320(2002).
 DR EMBL; AL606594; CAE01625.2; -;
 DR EMBL; AL606627; CAD41242.2; -;
 DR HSSP; P17707; 117B.
 DR Gramene; Q7X183; -;
 DR Gramene; Q7X183; -;
 DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
 DR GO; GO:0008295; P:spermidine biosynthesis; IEA.
 DR GO; GO:0006597; P:spermine biosynthesis; IEA.
 DR InterPro; IPR001985; SAM decarbox.
 DR Pfam; Pf01536; SAM decarbox; 1.
 DR ProDom; PD002379; SAM decarbox; 1.
 DR TIGRFAMs; TIGR00535; SAM_DCase; 1.
 DR PROSITE; PS01336; ADOMETDC; 1.
 SQ SEQUENCE 398 AA; 43283 MW; BC24F359962F8655 CRC64;
 Query Match 80.4%; Score 1538; DB 2; Length 398;
 Best Local Similarity 77.0%; Pred. No. 3.2e-120;
 Matches 308; Conservative 18; Mismatches 40; Indels 34; Gaps 5;
 QY 1 MAVLSAAGAPPASAIPEGVEKLEITFSEAPVDPHGSLRALRSQIDSVLDLAR-- 58
 DB 1 MGVLSAADPPVSAIPEGVEKLEITFSEAPVDPHGSLRALRSQIDSVLDLARCT 60
 QY 59 -----KIVIKTCGTTKLLTIPRIELAEBSMPLAAVKY 93
 DB 61 IVSELSNKFDSYVLSSESLFIYSKDIKVIKTCGTTKLLTIPRIELAEBSMPLAAVKY 120
 QY 94 SRGTFTPGQAQPHRSFSEVAVLNRYFGLKSGGNAYVIGDAARPGQKWHIYYATEP 153
 DB 121 SRGMFIPTSAQPHRSFSEVAVLNRYFGLKSGGNAYVIGDPAKPGQKWHIYYATQHP 180
 QY 154 EQPMVLEMCMTGLDTKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDPEPC 213
 DB 181 EQPMVLEMCMTGLDTKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDPEPC 240
 QY 214 GYSMNAIHGSAFTIHTVPDGFSGSYAEVWGLDATALSYGDLVXKRVLCFGSPFSVAV 273
 DB 241 GYSMNAIHGSAFTIHTVPDGFSGSYAEVWGLDATALSYGDLVXKRVLCFGSPFSVAV 300
 QY 274 TIFGGRGAQTGWKEIGAEAYDCNNMVVEQBLPGGILLIYQSCAAED--AVASSPKSVLR 331
 DB 301 TIFGGRGAQTGWKEIGAEAYDCNNMVVEQBLPGGILLIYQSCAAED--AVASSPKSVLR 360
 QY 332 CFPGD---NAAPAKCKLANVLCLEEXDAIEKDGVLDE 368
 DB 361 CFEAENMVNPAP-VKEGKGLNLLPWGE-DALEENDGVFDE 398
 RESULT 4
 DCAM_HORCH STANDARD; PRT; 393 AA.
 AC Q42829;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
 DE (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-
 DE adenosylmethionine decarboxylase beta chain].
 GN Name=SAMDC;
 OS Hordeum chilense (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=15565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96270739; PubMed=8639739;
 RA Dresselhaus T., Barcelo P., Hagel C., Loerz H., Humbeck K.;
 RA "Isolation and characterization of a Tritordeum cDNA encoding S-
 RT adenosylmethionine decarboxylase that is circadian-clock-regulated.";
 RL Plant Mol. Biol. 30:1021-1033(1996).
 CC -|- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (5-deoxy-5-
 CC adenosyl) (3-aminopropyl)-methylsulfonium salt + CO(2).
 CC -|- COFACTOR: Pyruvoyl group.
 CC -|- PATHWAY: Decarboxylation of S-adenosylmethionine provides the
 CC aminopropyl moiety required for spermidine and spermine
 CC biosynthesis from putrescine.
 CC -|- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X83881; CAAS8762.1; -;
 DR PIR; S69191; S69191.
 DR HSSP; P17707; 1JEN.
 DR InterPro; IPR001985; SAM decarbox.
 DR Pfam; Pf01536; SAM decarbox; 1.
 DR ProDom; PD002379; SAM decarbox; 1.
 DR TIGRFAMs; TIGR00535; SAM_DCase; 1.
 DR PROSITE; PS01336; ADOMETDC; 1.
 KW Decarboxylase; Lyase; Pyruvate; Spermidine biosynthesis; Zymogen.
 FT CHAIN 1 70
 FT S-adenosylmethionine decarboxylase beta
 FT chain (By similarity).
 FT CHAIN 71 393
 FT S-adenosylmethionine decarboxylase alpha
 FT chain (By similarity).
 FT SITE 70 71
 FT Cleavage (nonhydrolytic) (By similarity).
 FT MOD_RES 71 71
 FT Pyruvic acid (Ser) (By similarity).
 FT ACT_SITE 11 11
 FT By similarity.
 FT ACT_SITE 14 14
 FT By similarity.
 FT ACT_SITE 85 85
 FT By similarity.
 SQ SEQUENCE 393 AA; 42895 MW; 6CD1AA94792AF6CB CRC64;
 Query Match 76.9%; Score 1472.5; DB 1; Length 393;
 Best Local Similarity 74.6%; Pred. No. 9.5e-115;
 Matches 290; Conservative 25; Mismatches 43; Indels 31; Gaps 4;
 QY 9 APPASAIPEGVEKLEITFSEAPVDPHGSLRALRSQIDSVLDLAR----- 58
 DB 2 AAPVASIPEGVEKLEITFSEASIFADPHGRLALRSQAQIDSVLDLARCTTVSELSNK 61
 QY 59 -----KIVIKTCGTTKLLTIPRIELAEBSMPLAAVKYSGRTFIP 101
 DB 62 DFDVYVLSSESLFIYSKDIKVIKTCGTTKLLTIPRIELAEBSMPLAAVKYSGRTFIP 121
 QY 102 GAQPAPHRFSFSEVAVLNRYFGLKSGGNAYVIGDAARPGQKWHIYYATEYPPQMVNLE 161
 DB 122 GAQPAPHRFSFSEVAVLNRYFGLKSGGNAYVIGDPAKPGQKWHIYYATEYPPQMVNLE 181
 QY 162 MCMTGDLTKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDPEPCGYSMNAIH 221
 DB 182 MCMTGDLTKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDPEPCGYSMNAIH 241

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QY 222 GSASFTHVTPEDGFSYASVEVWGLDATALSYGLVKRVLCGFGSPSEFSAVAVTFGRGQ 281
Db 242 GSASFTHVTPEDGFSYASVEVWGLDATALSYGLVKRVLCGFGSPSEFSAVAVTFGRGH 301
QY 282 AGTWGKELGAEAYDCNNMVQEQLPGGGILLIYQSFCAEDAV--ASSPKSVLRFCFDG-ENA 338
Db 302 AATWGKLDREAYDCNNVVEQELPCGGVLLIYQSFANEELAVSAGSPRSVFHCFENVESG 361
QY 339 APPAFCKLANLVCL-EXDAIEBKGV 366
Db 362 HPLVKEGKLANLLAWRAEBSLEGTGAL 390

RESULT 5
Q92PJ1
ID Q92PJ1 PRELIMINARY; PRT; 392 AA.
AC Q92PJ1
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE S-adenosylmethionine decarboxylase.
OS Triticum aestivum (wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RA Li Z.Y., Chen S.Y.;
RT "Isolation and characterization of a salt and drought-inducible gene
RT for S-adenosylmethionine decarboxylase from wheat (Triticum aestivum
RT L.).";
RL J. Plant Physiol. 156:386-393 (2000).
DR EMBL; AF117660; AAD17232.1; -.
DR HSP; P17707; IJEN.
DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
DR GO; GO:0008295; P:permidine biosynthesis; IEA.
DR GO; GO:0006597; P:spermidine biosynthesis; IEA.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM DCase; 1.
DR PROSITE; PS01336; ADOMETC; 1.
SQ SEQUENCE 392 AA; 42854 MW; C761765631C2E91F CRC64;

Query Match 76.3%; Score 1460; DB 2; Length 392;
Best Local Similarity 74.5%; Pred. No. 1.1e-113;
Matches 287; Conservative 25; Mismatches 41; Indels 32; Gaps 4;

QY 9 APPASIGFEGYKRLITFSEAPVFDVPHGSLRALSRQIDSVLDLAR----- 58
Db 2 AAPTSAIGFEGYKRLITFSEASIFADPHGSLRALSRQIDSVLDLARCTTVSELSTK 61
QY 59 -----KIVIKTCGTTKLLTTPRILEAEELSMPLAAVKYSGVFIRP 101
Db 62 DPOSYVLSSESLFIYQKIVIKTCGTTKLLTTPRILEAEELSMPLAAVKYSGVFIRP 121
QY 102 GAQPAPHRSPSEEVAVLNRYFGGLKSGGNAYVIGDAARPGQKWHIYYATEYPPQMVNLE 161
Db 122 GAQPAPHRSPSEEVAVLNRYFGHLKSGGNAYVIGDPAKPGQKWHIYYATEYPPQMVNLE 181
QY 162 MCMTGLDTKASVFFKTNADGNTTCAKEMTKLSGISSEIIPEMEICDFDFPCGYSMAIH 221
Db 182 MCMTGLDKKASVFFKTDASHVSCAKEMTKLSGISDIIPEMEVCDPFPFCGYSMAIN 241
QY 222 GSASFTHVTPEDGFSYASVEVWGLDATALSYGLVKRVLCGFGSPSEFSAVAVTFGRGQ 281
Db 242 GSASFTHVTPEDGFSYASVEVWGLDATALSYGLVKRVLCGFGSPSEFSAVAVTFGRGH 301
QY 282 AGTWGKELGAEAYDCNNMVQEQLPGGGILLIYQSFCAEDAV--ASSPKSVLRFCFDG--N 337
Db 302 AATWGKLDREAYDCNNVVEQELPCGGVLLIYQSFANEELAVSAGSPRSVFHCFEASVH 361

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QY 338 AAPFAKCKLANLVCL-EXDAIEE 361
Db 362 SHPLVKEGKLANLLAWRAEEDSLEE 386

RESULT 6
Q6K9B8
ID Q6K9B8 PRELIMINARY; PRT; 395 AA.
AC Q6K9B8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE S-adenosylmethionine decarboxylase 2.
GN Name=OJ1476_F05.33; Synonyms=OJ1004_A05.7;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004063; BAD19232.1; -.
DR EMBL; AP005286; BAD19677.1; -.
DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
DR GO; GO:0008295; P:permidine biosynthesis; IEA.
DR GO; GO:0006597; P:spermidine biosynthesis; IEA.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM DCase; 1.
DR PROSITE; PS01336; ADOMETC; 1.
SQ SEQUENCE 395 AA; 43152 MW; 49C9BC56F20FB540 CRC64;

Query Match 76.2%; Score 1458; DB 2; Length 395;
Best Local Similarity 73.0%; Pred. No. 1.6e-113;
Matches 286; Conservative 25; Mismatches 47; Indels 34; Gaps 3;

QY 1 MAVLSAAGAPPASIGFEGYKRLITFSEAPVFDVPHGSLRALSRQIDSVLDLAR-- 58
Db 1 MAVLSVADSPPVSAIGFEGYKRLITFSEAPVFDVPHGSLRALSRQIDSVLDLARCT 60
QY 59 -----KIVIKTCGTTKLLTTPRILEAEELSMPLAAVKY 93
Db 61 IVSELSENEVDSVLSSESLFVVPYKIVIKTCGTTKLLTTPRILEAEELSMPLAAVKY 120
QY 94 SRGTFFPGAQAPHRSPSEEVAVLNRYFGGLKSGGNAYVIGDAARPGQKWHIYYATEY 153
Db 121 SRGTFFPGAQSPHPNFSEEVAVLNRYFGGLKSGGNAYVIGDPAKPGQKWHIYYATQHP 180
QY 154 EQPMVNLWCMTGLDTKASVFFKTNADGNTTCAKEMTKLSGISSEIIPEMEICDFDFPC 213
Db 181 EQPVVTLWCMTGLDKKASVFFKTSADGHTTAKEMTKLSGISDIIPEMEVCDPFPFC 240
QY 214 GYSMNAIHGSAFSTIHTVTPEDGFSYASVEVWGLDATALSYGLVKRVLCGFGSPSE 273
Db 241 GYSMNAIHGSAFSTIHTVTPEDGFSYASVEVWGLDATALSYGLVKRVLCGFGSPSE 300
QY 274 TIFGGRGQAGTWGKELGAEAYDCNNMVQEQLPGGGILLIYQSFCAEDAVASSPKSVLR 333
Db 301 TIFGGRNHAGTWGKLDVGVGSCSNVVEQELPSGGLLIYQSFATAEIAIATGSPRSV 360
QY 334 DGENAAPFAKCKLANLVCL-EXDAIEBKDG 364
Db 361 ADENTE-----KAGKMEALYWDDEAVEIDG 386

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RESULT 7

Q6F4N6 PRELIMINARY; PRT; 395 AA.

AC Q6F4N6; 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE S-adenosylmethionine decarboxylase.

GN Name=SAMDCL1; Synonym=P0418B08.27-1;

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzaceae; Oryza.

OX NCBI_TaxID=4530;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21066059; PubMed=11139406; DOI=10.1042/0264-6021.3530403;

RA Franceschetti M., Hanfrey C., Scaramagli S., Torrigiani P., Bagni N.,

RA Michael A.J.;

RT "Characterization of moncot and dicot plant S-adenosyl-methionine

RT decarboxylase gene families including identification in the mRNA of a

RT highly conserved pair of upstream overlapping open reading frames.";

RL Biochem. J. 353:403-409(2001).

DR EMBL; AJ251899; CAB64600.1; -.

DR HSSP; P17707; IJEN.

DR Gramene; Q9SC67; -.

DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.

DR GO; GO:0016829; F:lyase activity; IEA.

DR GO; GO:0008295; P:spermidine biosynthesis; IEA.

DR GO; GO:0006597; P:spermine biosynthesis; IEA.

DR InterPro; IPR001985; SAM decarbox.

DR Pfam; PF01536; SAM decarbox; 1.

DR ProDom; PD002379; SAM decarbox; 1.

DR TIGRFAMs; TIGR00535; SAM DCase; 1.

DR PROSITE; PS01336; ADOMETDC; 1.

KW Lyase.

SQ SEQUENCE 395 AA; 43152 MW; 49C9BC56F20FE540 CRC64;

Query Match 76.2%; Score 1458; DB 2; Length 395;

Best Local Similarity 73.0%; Pred. No. 1.6e-113;

Matches 286; Conservative 25; Mismatches 47; Indels 34; Gaps 3;

QY 1 MAVLSAAGAPPASAIPEGYKELEITFSAPVFDPHGSLRALSQIDSVDLRLAR-- 58

DB 1 MAVLSVADSPVPSAIGPEGYKELEITFSAPVFDPHGSLRALSQIDSVDLRLARCT 60

QY 59 -----KIVIKTCGTTKLLTIPRILELAELSPLAAYKY 93

DB 61 IVSELSNEVDSYVLSSESLFVYPIKIVIKTCGTTKLLLAIPRILELAELSPLAAYKY 120

QY 94 SRTGTFIPGAQAPAPHSFSEVAVLNRYFGGLSGGNAYVIGDAAPGQKWHIYYATEYP 153

DB 121 SRTGTFIPGAQAPAPHSFSEVAVLNRYFGGLSGGNAYVIGDAAPGQKWHIYYATQHP 180

QY 154 EQPMVNLWCMTGLDTPKASVFFKTNADGNNTTCAKEMTKLSGISEIIPEMEICDFDFEPC 213

DB 181 EQPVTLEMCMTGLDKKASVFFKTSADGHTTAKEMTKLSGISDIIPEMEVCDFDFEPC 240

QY 214 GYSMNAIHGSAFSTIHTVPDGFYSASYEVWGLDATALSYGDLVKRVLGCGFSGSEFSVAV 273

DB 241 GYSMNAIHGSAFSTIHTVPDGFYSASYEVWGLDATALSYGDLVKRVLGCGFSGSEFSVAV 300

QY 274 TIFGGRQAGTWCKELGAEAYDCNNMVEQLPGGILLIYOSFCAAEADVASSPKSVLRCP 333

DB 301 TIFGGRNAGTWCKELGAEAYDCNNMVEQLPGGILLIYOSFCAAEADVASSPKSVLRCP 360

QY 334 DGENAAPFAKCKLANLVCLLEEXDAIEEKD 364

DB 361 ADENTE-----KAGKMEALYWDVDAVEIDG 386

RESULT 8

Q6F4N6

Q6F4N6 PRELIMINARY; PRT; 392 AA.

AC Q6F4N6; 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE S-adenosylmethionine decarboxylase.

GN Name=SAMDCL1; Synonym=P0418B08.27-1;

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzaceae; Oryza.

OX NCBI_TaxID=39947;

RN [1]

RP SEQUENCE FROM N.A.

RX PubMed=15215597;

RA Yamaguchi T., Nakayama K., Hayaashi T., Yazaki J., Kishimoto N.,

RA Kikuchi S., Koike S.;

RT "cDNA Microarray Analysis of Rice Anther Genes under Chilling Stress

RT at the Microsporogenesis Stage Revealed Two Genes with DNA Transposon

RT Castaway in the 5'-Flanking Region.";

RL Biosci. Biotechnol. Biochem. 68:1315-1323(2004).

RN [2]

RP SEQUENCE FROM N.A.

RA Sasaki T., Matsumoto T., Katayose Y.;

RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, PAC

RT clone: P0418B08.";

RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB122089; BAD26704.1; -.

DR EMBL; AF005420; BAD33432.1; -.

DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.

DR GO; GO:0008295; P:spermidine biosynthesis; IEA.

DR GO; GO:0006597; P:spermine biosynthesis; IEA.

DR InterPro; IPR001985; SAM decarbox.

DR Pfam; PF01536; SAM decarbox; 1.

DR ProDom; PD002379; SAM decarbox; 1.

DR TIGRFAMs; TIGR00535; SAM DCase; 1.

DR PROSITE; PS01336; ADOMETDC; 1.

SQ SEQUENCE 392 AA; 42717 MW; 0DF1F61522C38FE3 CRC64;

Query Match 65.0%; Score 1244; DB 2; Length 392;

Best Local Similarity 62.6%; Pred. No. 1.3e-95;

Matches 244; Conservative 48; Mismatches 68; Indels 30; Gaps 3;

QY 1 MAVLSAAGAPPASAIPEGYKELEITFSAPVFDPHGSLRALSQIDSVDLRLAR-- 58

DB 3 MSLADSWGAPASPIGPEGYKELEITLSDAPVFDPCGRLALREQIDSLDLAKCT 62

QY 59 -----KIVIKTCGTTKLLTIPRILELAELSPLAAYKY 93

DB 63 IVSHLSNKHFDSDYVLSSESLFVYPIKIVIKTCGTTKLLLAIPRILELAELSPLAAYKY 122

QY 94 SRTGTFIPGAQAPAPHSFSEVAVLNRYFGGLSGGNAYVIGDAAPGQKWHIYYATEYP 153

DB 123 SRGMFIPGAQAPAPHSFSEVAVLNRYFGGLSGGNAYVIGDAAPGQKWHIYYATEEP 182

QY 154 EQPMVNLWCMTGLDTPKASVFFKTNADGNNTTCAKEMTKLSGISEIIPEMEICDFDFEPC 213

DB 183 EQPVTLEMCMTGLDKKASVFFKTSADGHTTAKEMTKLSGISEIIPEMEICDFDFEPC 242

QY 214 GYSMNAIHGSAFSTIHTVPDGFYSASYEVWGLDATALSYGDLVKRVLGCGFSGSEFSVAV 273

DB 243 GYSMNGIYGPVASTIHTVPDGFYSASYEVWGLDATALSYGDLVKRVLGCGFSGSEFSVAV 302

QY 274 TIFGGRQAGTWCKELGAEAYDCNNMVEQLPGGILLIYOSFCAAEADVASSPKSVLRCP 333

DB 303 TIFGGRHAGTWCKELGAEAYDCNNMVEQLPGGILLIYOSFCAAEADVASSPKSVLRCP 361

QY 334 DGENAAPFAKCKLANLVCLLEEXDAIEEKD 363

DB 362 NSDGAERWAKSKEMS--VCWEGEKAACKKD 389

RESULT 9

Q84LA2 PRELIMINARY; PRT; 370 AA.
 ID Q84LA2
 AC Q84LA2
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE S-adenosylmethionine decarboxylase.
 GN Name=Samdc;
 OS Narcissus pseudonarcissus (Daffodil).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;
 OC Narcissus.
 OX NCBI_TaxID=39639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=4-day old flower tepals;
 RA Gookin T.E., Cabauatan E.V., Hunter D.A., Reid M.S.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY232672; AAC043186.1; -;
 DR HSP; P17707; 1JEN
 DR GO; GO:0004014; P:adenosylmethionine decarboxylase activity; IEA.
 DR GO; GO:0008295; P:spemidine biosynthesis; IEA.
 DR GO; GO:0006597; P:spemidine biosynthesis; IEA.
 DR InterPro; IPR001985; SAM decarbox.
 DR Pfam; PF01536; SAM decarbox; 1.
 DR ProDom; PD002379; SAM decarbox; 1.
 DR TIGRFAMS; TIGR00535; SAM DCase; 1.
 DR PROSITE; PS01336; ADOMETDC; 1.
 SQ SEQUENCE 370 AA; 40680 MW; 36F619BA4806F70F CRC64;
 Query Match 62.0%; Score 1187.5; DB 2; Length 370;
 Best Local Similarity 60.7%; Pred. No. 6.5e-91; Indels 43; Gaps 3;
 Matches 229; Conservative 48; Mismatches 57;
 QY 13 SAIGFEGYKRLITFEAPVFDVPHGSGRLALRSQIDSILDLAR----- 58
 DB 7 SPIGFEGYKRLITFEASAFVDPHGRGLRALRSQIDSILDLARCTIVDHLNKKDFDS 66
 QY 59 -----KIVIKTCGTTKLLTIPRIELAEBSMPLAAVKYSGRTIFFGAQP 105
 DB 67 YVLSSESLFYVPCMKILKTCGTTLLLSIPVILDLAELSLSVTAVKYSRGSFIFFGAQP 126
 QY 106 AHRSPSEEVAVLNRYFGGLKSGNAYVIGDAARPGQKHYYVATEYPEOPMNVLECMT 165
 DB 127 TPRNPFSEVSLDHFPGNLASGNAYVIGDPSPNRWHYYATQPELPTVTLECMT 186
 QY 166 GLDTKASVFFKTNADGNTTCAKEMTKLSGISIIPMEICDFDFPCGYSMNAIHGSF 225
 DB 187 GLDSEKASIFFNPGNANNAQSKMTKLSGISNIIPMEICDFDFPCGYSMNAICGSAH 246
 QY 226 STIHVTPEDGFSYASVEVMGLDATALSYGLVKRVLCGFPSPFSVAVTIFGGRGQAGTW 285
 DB 247 STIHVTPEDGSSYASVEAMGNFAELDFGGLVERVLECFGPAFSAVTIFGGRGQAGSW 306
 QY 286 GKELGAEAYDCNNMVQELPGGGLIYQSCAAEDAVASSPKSVLCRFDGENAAPFAKDC 345
 DB 307 GREVDVSGFRCVLDVLEQELAGGGLIMYQSFAGVGRM-GSPRSTLHCWDGEE----- 357
 QY 346 KLANVLCLEEXDAIEEK 362
 DB 358 -----IEEKAEDKK 367
 RESULT 10
 Q944U3 PRELIMINARY; PRT; 369 AA.
 ID Q944U3
 AC Q944U3
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE S-adenosyl-L-methionine decarboxylase.
 GN Name=Samdc;
 OS Dendrobium crumenatum (Tropical pigeon orchid).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
 OC Epidendroideae; higher Epidendroideae; Dendrobieae; Dendrobieinae;
 OC Dendrobium.
 OX NCBI_TaxID=51096;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Han P., Pua E.C.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF420239; AAL16065.1; -;
 DR HSP; P17707; 1JEN
 DR GO; GO:0004014; P:adenosylmethionine decarboxylase activity; IEA.
 DR GO; GO:0008295; P:spemidine biosynthesis; IEA.
 DR GO; GO:0006597; P:spemidine biosynthesis; IEA.
 DR InterPro; IPR001985; SAM decarbox.
 DR Pfam; PF01536; SAM decarbox; 1.
 DR ProDom; PD002379; SAM decarbox; 1.
 DR TIGRFAMS; TIGR00535; SAM DCase; 1.
 DR PROSITE; PS01336; ADOMETDC; 1.
 SQ SEQUENCE 369 AA; 40635 MW; 48E8ECB19BA2EAE3 CRC64;
 Query Match 60.8%; Score 1160; DB 2; Length 369;
 Best Local Similarity 58.9%; Pred. No. 1.3e-88;
 Matches 224; Conservative 58; Mismatches 50; Indels 48; Gaps 4;
 QY 13 SAIGFEGYKRLITFEAPVFDVPHGSGRLALRSQIDSILDLAR----- 58
 DB 4 SPIGFEGYKRLITFEAPLFVDPHGRGLRALRTPQIDSILDLARCTIVSLSNKHFD 63
 QY 59 -----KIVIKTCGTTKLLTIPRIELAEBSMPLAAVKYSGRTIFFGAQP 105
 DB 64 YVLSSESLFYVPCMKILKTCGTTLLLSIPVILDLAELSLSVTAVKYSRGSFIFFGAQP 123
 QY 106 AHRSPSEEVAVLNRYFGGLKSGNAYVIGDAARPGQKHYYVATEYPEOPMNVLECMT 165
 DB 124 AHRSPSEEVAVLNRYFGGLKSGNAYVIGDPAHPNLNWHVYVASEKPEQPMVTIEMCMT 183
 QY 166 GLDTKASVFFKTNADGNTTCAKEMTKLSGISIIPMEICDFDFPCGYSMNAIHGSF 225
 DB 184 GLNTEKASIFFKNSVPRHSSAKEMTKRSKICDIIPEMKICDFDFPCGYSMNGINKAL 243
 QY 226 STIHVTPEDGFSYASVEVMGLDATALSYGLVKRVLCGFPSPFSVAVTIFGGRGQAGTW 285
 DB 244 STIHVTPEDGFSYASVEAMGNFAELDFGGLVERVLECFGPAFSAVTIFGGRPFACS 303
 QY 286 GKELGAEAYDCNNMVQELPGGGLIYQSCAAEDAVASSPKSVLCRFDGENAAPFAKDC 345
 DB 304 GKQSVNGYCNCKNLVQDLGGGLLYQSPKASDGG-SASPRSLYCWAE-----AED- 356
 QY 346 KLANVLCLEEXDAIEEKGV 365
 DB 357 -----EEENG 362
 RESULT 11
 Q9FSM2 PRELIMINARY; PRT; 319 AA.
 ID Q9FSM2
 AC Q9FSM2
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE S-adenosylmethionine decarboxylase.
 GN Name=H0711G06.28;
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Han B., Peng Q., Mu J., Zhou B., Chen Z.H., Li Y., Zhu J.J.,
 RA Tang Y.S., Zhao Q., Liu Y.L., Huang Y.C., Yu Z., Fan D.L., Chen L.,
 RA Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Zhu J., Liu X.H., Hu X.,

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RA Lei H.Y., Zhang Y.J., Wang R., Li C., Lu Y., Chen X.C., Zhang Y.,
RA Hu H., Jia P.X., Li T., Qian Y.M., Ying K., Hong G.F.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL442115; CAC09522.1; -.
DR HSP; P17707; I17B.
DR Gramene; Q9FSW2; -.
DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
DR GO; GO:0008295; P:spermidine biosynthesis; IEA.
DR GO; GO:0006597; P:spermine biosynthesis; IEA.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM_Dcase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
SQ SEQUENCE 319 AA; 34854 MW; B0648B852F7A4AE1 CRC64;

Query Match 59.38; Score 1134.5; DB 2; Length 319;
Best Local Similarity 80.28; Pred. No. 1.5e-86;
Matches 223; Conservative 10; Mismatches 18; Indels 27; Gaps 1;

QY 1 MAVLSAAGAPPASAIPEGYEKRLIITFSEAPVFDPHGSLRALRSQIDSVLDLAR-- 58
DB 37 MGVLAAADPPVPSAIGPEGYEKRLIITFSEAPVFDPHGSLRALRSQIDSVLDLARCT 96
QY 59 -----KIVIKTGGTTKLLLTIPRILELAELSMPLAAYKVSRTGTFEP 101
DB 62 IVDSYVLSSESLFVYPYKIIKTCGTTKLLLTIPRILELAELSMPLAAYKVSRTGTFEP 121
QY 102 GAQPAPHRFSERVAVNLRYFGLKSGGNAYVIGDAARPCQKWHIY-YATEYP--EQPMV 158
DB 122 GAQYPRHFSERVAVLDGHFELGAGSKAYVMGSHDKP-QKWHVYTAATAAEFTGRSDPY 180
QY 159 NLEMCWTGLDTKASVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDFDFPCGYSMN 218
DB 181 TLEMCMTGLDRKKAASVFKT-----DTSSAAVMTENGIRKILPNSIETCDFEPCGYSMN 236
QY 219 AIHGSASFSTIHTVPEDGFSYASVEVMGLDATALSYGDLVKRVLGCGPSESFAVTTIFGG 278
DB 237 AIEGAISTIHVTPEGFSYASVETVGNPKVNLSHLIERVLSFCQPNSEFSAV----- 291
QY 279 RGQAGTWGK-----ELGAEAYDCNNVVEOLPGGILIIYQSFCAAEADAVASPKSVLRC 332
DB 292 --HADISGKLLERCLLDVKGCCERSNEELGCMGSMVYHRFMKTEGLV--SPRSILKC 347

RESULT 12
Q7XZQ9 PRELIMINARY; PRT; 358 AA.
AC Q7XZQ9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50).
GN Name=samdc;
OS Vitis vinifera (Grape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Vitaceae; Vitis.
OX NCBI_TaxID=29760;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Tassoni A., Accetulli P., Bagni N.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ567368; CAD98785.1; -.
DR HSP; P17707; IJEN.
DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008295; P:spermidine biosynthesis; IEA.
DR GO; GO:0006597; P:spermine biosynthesis; IEA.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM_Dcase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
KW Lyase.
FT CHAIN 2 358 S-adenosylmethionine decarboxylase.

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DR EMBL; U12573; AAC48989.1; -.
DR PIR; S68990; S68990.
DR HSP; P17707; IJEN.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM DCase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
KW Decarboxylase; Lyase; Pyruvate; Spermidine biosynthesis; Zymogen.
FT CHAIN 1 70
FT S-adenosylmethionine decarboxylase beta
FT chain.
FT CHAIN 71 357
FT S-adenosylmethionine decarboxylase alpha
FT chain.
FT SITE 70 71
FT Cleavage (nonhydrolytic).
FT MOD_RES 71 71
FT Pyruvic acid (Ser).
FT ACT_SITE 11 11
FT By similarity.
FT ACT_SITE 14 14
FT By similarity.
FT ACT_SITE 85 85
FT By similarity.
FT MUTAGEN 71 71
FT S->A: Loss of activity.
SQ SEQUENCE 357 AA; 39714 MW; 364918E116388301 CRC64;

Query Match 44.5%; Score 854.5; DB 1; Length 357;
Best Local Similarity 47.6%; Pred. No. 4.8e-63;
Matches 185; Conservative 52; Mismatches 83; Indels 69; Gaps 8;

QY 9 APPASAIIGFEGYKRLITSEAPVFDVPHGSGLRALSRQIDSVLRLAR----- 58
DB 2 ALPASAIGFEGYKRLITSEAPVFDVPHGSGLRALSRQIDSVLRLAR----- 61
QY 59 -----KIVIKCTGTTKLLTTPRILELAELSMPAAVKYRGTFIFP 101
DB 62 YLDSYVLSSESLFVYVKIITKCTGTTKLLTTPAILKLAESLSVRNVKTRGSFIFP 121
QY 102 GAGAPHRSESEVAVLNRYFGGLKSGGNAYVIGDAARPCQKHYYATYPRQ----PMV 158
DB 122 GAQSFPHRSSEVELLDNRYFGGLKSGGNAYVIGDAARPCQKHYYATYPRQ----PMV 180
QY 159 NLEWCMCTGLTKKASVFEKTNADGNTTCAKEMTKLSGISIIPEMEICDFDPFCGYSMN 218
DB 181 TLEWCMCTGLTKKASVFEKTNADGNTTCAKEMTKLSGISIIPEMEICDFDPFCGYSMN 236
QY 219 AIHGSAPSTHTVTPEDGFSYASVEVMGLDATALSYGLVKRVLCGFGPSEFSAVTIFGG 278
DB 237 SIEEAALSTHTVTPEDGFSYASVEVMGLDATALSYGLVKRVLCGFGPSEFSAVTIFGG 291
QY 279 RQAGATGK-----ELGAEAYDCNNVVEQLPGGILYIYQSCAAEDAVASPKSVLRC 332
DB 292 --HCDVTCKSLQICSLKELKEYSLDEKINEELGLGGSIIYKFLRID--ACGSPRSILKC 347
QY 333 FDGENAAPFAKCKLANLVGLEEXDAIEE 361
DB 348 -----CWKEDESEEE 357

RESULT 14
DCAM_VICFA
ID _DCAM_VICFA STANDARD; PRT; 353 AA.
AC Q9M4DB;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdometDC)
DE (SamDC) [contains: S-adenosylmethionine decarboxylase alpha chain; S-
DE adenosylmethionine decarboxylase beta chain].
GN Name=SAMDC;
OS Vicia faba (Broad bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.
OX NCBI_TaxID=3906;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Kleine Thueringer; TISSUE=Root nodules;
```

DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
DE (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-
DE adenosylmethionine decarboxylase beta chain].
GN Name=SAMDC;
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Monatol;
RC MDLINE=95288374; PubMed=7770535; DOI=10.1104/pp.107.4.1461;
RA Bolle C., Herrmann R.G., Oelmüller R.;
RT "A spinach cDNA with homology to S-Adenosylmethionine decarboxylase";
RL Plant Physiol. 107:1461-1462(1995).
CC -|- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S-deoxy-5-
CC adenosyl)(3-aminopropyl)-methylsulfonium salt + CO(2).
CC -|- COFACTOR: Pyruvoyl group (By similarity).
CC -|- PATHWAY: Decarboxylation of S-adenosylmethionine provides the
CC aminopropyl moiety required for spermidine and spermine
CC biosynthesis from putrescine.
CC -|- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X81414; CAA57170.1; --
DR PIR; S49222; S49222.
DR HSSP; P17707; IJEN.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM_DCase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
KW Decarboxylase; Lyase; Pyruvate; Spermidine biosynthesis; Zymogen.
FT CHAIN 1 68 S-adenosylmethionine decarboxylase beta
FT chain (By similarity).
FT CHAIN 69 363 S-adenosylmethionine decarboxylase alpha
FT chain (By similarity).
FT SITE 68 69 Cleavage (nonhydrolytic) (By similarity).
FT MOD_RES 69 69 Pyruvic acid (Ser) (By similarity).
FT ACT_SITE 9 9 By similarity.
FT ACT_SITE 12 12 By similarity.
FT ACT_SITE 83 83 By similarity.
SQ SEQUENCE 363 AA; 39959 MW; CE4D6DDE4E8A3220 CRC64;
Query Match 43.9%; Score 841; DB 1; Length 363;
Best Local Similarity 46.6%; Pred. No. 6.6e-62;
Matches 184; Conservative 45; Mismatches 86; Indels 80; Gaps 9;
QY 13 SAIGFEGYKRLRITTFSEAPVFVDPHGSLRALRSQIDSVDL----- 55
DB 4 SAIGFEGFKRLRITTFEPSPFIFVDPEGLRALCAQLDEILGPAECTIVDSLANSVDS 63
QY 56 -----LARKIVIKTGTGTLTLTIPRIELAEELSMPLAAVKYSGTIFPCAOP 105
DB 64 YVLSSESLFYAYKIIITCGTKLRAIPPLRLACKLSLVKSVRYTRGSFIFPGAQS 123
QY 106 APHRSFSEEVAVLNRYFGGLKSGNAVYIGDAPRPGOKWHYYATEYP---EOPMVNLEM 162
DB 124 YAHRSFSEEVAVLDYFGKLAAGSKAFVWGDPKAP-QXNVHVSASAEITISFEFVYILEM 182
QY 163 CMTGLDTKASVFFKTNADGNNTTCAKEMTKLSGISEIIPEMEICDPDFPCGYSMNAIHG 222
DB 183 CMTGLKKEKASVFFPKSPN-----AAVMTESSGIRKILPDSKICDPDFPCGYSMNAIEG 238

QY 223 SAFSTIHVTPEDGFSYASYEVVMGLDATALSYGLVKRVLCGFGPSEFSVAVTIFGSRGQA 282
DB 239 PAISTIHITPEDGFSYASFEAVGYDLKTKDNLQVERVLACFPSPSEFSIAI----- 289
QY 283 GTWKGELGAEAYDCNNMVE-----QELP-GGGILLYQSFCAAED--AVASSPKS 328
DB 290 ---HAEIAANSMEHNHCYVNVNGYSRBEGGIEELGFGAASVYQKFKCASTGFGATNPKP 346
QY 329 VLRCFDGNAAPFAKDKCLANLYCLEEXDAIEBKD.363
DB 347 ALKC-----CWKEDKFEEEKD 362

Search completed: May 11, 2005, 22:52:29
Job time : 87.9416 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2005, 22:42:53 ; Search time 19.6014 Seconds
(without alignments)
1806.392 Million cell updates/sec

Title: US-10-732-923-407

Perfect score: 1914

Sequence: 1 MAVLSAAGAPPASAIQFEGY.....NLVCLREXDAIEKQGVLD 368

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1726	90.2	400	2 T03947	adenosylmethionine
2	1520	79.4	398	2 T04099	adenosylmethionine
3	1472.5	76.9	393	2 S69191	adenosylmethionine
4	854.5	44.6	357	2 S68990	adenosylmethionine
5	841	43.9	363	2 S49222	adenosylmethionine
6	837.5	43.8	361	2 T01934	adenosylmethionine
7	834	43.6	353	2 T06515	probable adenosylm
8	825.5	43.1	381	2 T10707	adenosylmethionine
9	824.5	43.1	377	2 T10708	adenosylmethionine
10	822.5	43.0	360	2 S52662	adenosylmethionine
11	763.5	39.9	361	2 T12613	adenosylmethionine
12	757	39.6	362	2 T51378	adenosylmethionine
13	751	39.2	369	2 T10750	probable adenosylm
14	377.5	19.7	368	2 T22361	adenosylmethionine
15	359.5	18.8	334	1 DCHYDM	adenosylmethionine
16	357.5	18.7	334	2 A55948	adenosylmethionine
17	356.5	18.6	334	1 DCHUDM	adenosylmethionine
18	351.5	18.4	333	1 DCRDTM	adenosylmethionine
19	337.5	17.6	335	2 S72197	adenosylmethionine
20	294	15.4	396	1 DCBIDM	adenosylmethionine
21	99.5	5.2	2297	2 T34918	polyketide synthase
22	96.5	5.0	410	2 AH3376	glycosyltransferase
23	95.5	5.0	357	2 JQ0118	acyl-CoA-6-aminope
24	94.5	4.9	1307	2 T35944	probable beta-gala
25	90.5	4.7	689	2 F81286	probable polysacch
26	90.5	4.7	3972	2 S75251	hypothetical prote
27	90	4.7	288	2 H95274	probable ABC trans
28	90	4.7	1354	2 T13363	phosphoribosylform
29	89.5	4.7	656	2 A33483	dnaK-type molecula

30	89	4.6	255	2 H75074	lactam utilization
31	89	4.6	774	2 B84031	ATP-dependent prot
32	88.5	4.6	719	2 A42808	lg light chain-bin
33	88	4.6	352	2 C90547	oligopeptide ABC t
34	88	4.6	355	2 T50566	probable ABC-type
35	88	4.6	433	2 T36609	probable secreted
36	88	4.6	983	2 AG2381	glycine cleavage s
37	87.5	4.6	255	1 E71090	probable lactam ut
38	87.5	4.6	759	2 B3749	probable formate d
39	87	4.5	534	2 B97352	polygalacturonase
40	86.5	4.5	739	2 H72364	aspartokinase II -
41	86.5	4.5	1397	2 A85570	rhaC protein in rh
42	86.5	4.5	1397	2 C64805	rhaC protein precu
43	86.5	4.5	1431	2 A45866	dextranucrase (EC
44	86	4.5	355	2 F69298	conserved hypotet
45	86	4.5	374	2 C91198	BspD protein limpo

ALIGNMENTS

RESULT 1

T03947

adenosylmethionine decarboxylase (EC 4.1.1.50) - maize

N/Alternate names: S-adenosylmethionine decarboxylase

C/Species: Zea mays (maize)

C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C/Accession: T03947

R/Michael, A.J.

submitted to the EMBL Data Library, September 1996

A/Reference number: Z15155

A/Accession: T03947

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-400 <MIC>

A/Cross-references: UNIPROT:O24575; EMBL:Y07767; PIDN:CAA69075.1

C/Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type

C/Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase

F/78/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 90.2%; Score 1726; DB 2; Length 400;
Best Local Similarity 84.5%; Pred. No. 2.56-135;
Matches 338; Conservative 8; Mismatches 22; Indels 32; Gaps 3;

Qy 1 MAVLSAAGAPPASAIQFEGYEKLEITFSEAPVFPVPHGSLRALSRQSDSVLDLAR-- 58

Db 1 MAVLSAADASPVSAIGFEGYEKLEITFSEAPVFPVPHGSLRALSRQSDSVLDLARCT 60

Qy 59 -----KIVIKTCGTTKLLTIPRILELAELSMPAAVKY 93

Db 61 IVSELNKKDFDSVYLSSESLFIYPLKIVIKTCGTTKLLTIPRILELAELSMPAAVKY 120

Qy 94 SRGTFFPGQAPHRSPSEVAVLNRYFGGLSGGNAYVIGDAARPGQKWHYAYTEYP 153

Db 121 SRGTFFPGQAPHRSPSEVAAALNRYFGGLSGGNAYVIGDPAREGQKWHYAYTEYP 180

Qy 154 EQPMVNLNEMCTGLDTPKASVRFKTNADGNNTTCAKEMTKLSGISEIIPENICDPDFEPC 213

Db 181 EQPMVNLNEMCTGLDKKKACVFFKTNADGNNTTCAKEMTKLSGISEIIPENICDPDFEPC 240

Qy 214 GYSMNAIHGSAFTIHTVPEDGFSYASYEVMGLDATALSYGDLVKRVLRCFGSFSFSAV 273

Db 241 GYSMNAIHGSAFTIHTVPEDGFSYASYEVMGLDATALSYGDLVKRVLRCFGSFSFSAV 300

Qy 274 TIFGGRGAGTGWKELGAEAYDCNNMVVEQLPGGGLIYQSFCAAEADAVASSPKSVURCF 333

Db 301 TIFGGRGAGTGWKELGAEAYDCNNMVVEQLPGGGLIYQSFCAAEADAVASSPKSVURCF 360

Qy 334 DGENA-----APPAKDKLANLVCL-REXDAIEBKQGVLD 368

Db 361 DGENVSAPPMMKKDYKLANLVCL-REXDAIEBKQGVLD 400

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RESULT 2
T04099
adenosylmethionine decarboxylase homolog [similarity] - rice
C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Mar-2004
C;Accession: T04099
R;Michael, A.J.
submitted to the EMBL Data Library, September 1996
A;Description: Spermidine biosynthesis in rice.
A;Reference number: Z15210
A;Accession: T04099
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-398 <MC>
A;Cross-references: EMBL:Y07766; PIDN:CAA69074.1
A;Experimental source: cv. Nipponbare
A;Note: this sequence appears to lack the residues necessary to form an active site
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type

Query Match      79.4%; Score 1520; DB 2; Length 398;
Best Local Similarity 76.5%; Pred. No. 3e-118;
Matches 306; Conservative 18; Mismatches 42; Indels 34; Gaps 5;

Qy 1 MAVLSAAGAPASGAIGFEGYKRLIETFSAPVFDVPHGSGLRALSRSQIDSVLDLAR-- 58
Db 1 MGDLSAADPPVSAIGFEGYKRLIETFSAPVFDVPHGSGLRALSRSQIDSVLDLARCT 60

Qy 59 -----KIVIKTCGTTKLLLTTPRILELAELSMPPLAAVKY 93
Db 61 IVSELSNKDFSVLLSPACLSILIKIVIKTCGTTKLLLTTPRILELAELSMPPLAAVKY 120

Qy 94 SRGTIFPGQAPAPHRFSSEVAVLNRYFGLKSGGNAYVIGDAARPGQKWHIYYATEYP 153
Db 121 SRGFIFFPSAQPAPLRSFSEVAVLNRYFGLKSGGNAYVIGDPAKPGQKWHIYYATQHP 180

Qy 154 EQPMVNLMECWTGLDITKASVFFKTNADGNTTCAKEMTKLSGISIIPMEICDFDFPEPC 213
Db 181 EQPMVNLMECWTGLDITKASVFFKTSADGHTSCAKEMTKLSGISIIPMEICDFDFPEPC 240

Qy 214 GYSNNAIHGSAFTIHTVTPEDGFSYASYEVNGLDATALSYGDLVKRLVLCGFGSFSVAV 273
Db 241 GYSNNAIHGSAFTIHTVTPEDGFSYASYEVNGLDATALSYGDLVKRLVLCGFGSFSVAV 300

Qy 274 TIFGRCQAGTWKELCAEAYDCNNMVEQELPGGILLIYQSFCAED--AVASPKSVLR 331
Db 301 TIFGHHGAGTWKELNADAYKCNNMVEQELPGCGLLIYQSFDAEDVPVAVGSPKSVLH 360

Qy 332 CFDGE---NAAPFAKCKLANLVCLLEKDAIEEKDGVLD 368
Db 361 CFEAENMVPAP-VKEGKLGKLLPWGE-DALENDGVFDE 398

RESULT 3
S69191
adenosylmethionine decarboxylase (EC 4.1.1.50) precursor - wild barley
C;Species: Hordeum chilense (wild barley)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S69191
R;Dresselhaus, T.; Barcelo, P.; Hagel, C.; Loerz, H.; Humbeck, K.
Plant Mol. Biol. 30, 1021-1033, 1996
A;Title: Isolation and characterization of a Tritordeum cDNA encoding S-adenosylmethionine
A;Reference number: S69191; MUID:96270379; PMID:8639739
A;Accession: S69191
A;Molecule type: mRNA
A;Residues: 1-393 <DRE>
A;Cross-references: UNIPROT:Q42829; EMBL:X83881; NID:g1403043; PIDN:CAA58762.1; PID:g140
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;1-71/Product: adenosylmethionine decarboxylase beta chain #status predicted <MAT1>
F;72-393/Product: adenosylmethionine decarboxylase alpha chain #status predicted <MAT2>
F;247-262/Region: PEST sequence
F;71/Modified site: pyruvic acid (Ser) (in mature form) #status predicted
```

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Query Match      76.9%; Score 1472.5; DB 2; Length 393;
Best Local Similarity 74.6%; Pred. No. 2.6e-114;
Matches 290; Conservative 25; Mismatches 43; Indels 31; Gaps 4;

Qy 9 APPASAI GFEGYKRLIETFSAPVFDVPHGSGLRALSRSQIDSVLDLAR----- 58
Db 2 AAPVASI GFEGYKRLIETFSAPVFDVPHGSGLRALSRSQIDSVLDLARCTIVSELSNK 61

Qy 59 -----KIVIKTCGTTKLLLTTPRILELAELSMPPLAAVKYRGRTIFFP 101
Db 62 DFDYVLSSESLFIYSQKIVIKTCGTTKLLLTTPRILELAELSMPPLAAVKYRGRTIFFP 121

Qy 102 GAOPAPHRFSSEVAVLNRYFGLKSGGNAYVIGDAARPGQKWHIYYATEVPQPMVNL 161
Db 122 GAOPAPHRFSSEVAVLNRYFGLKSGGNAYVIGDPAKPGQKWHIYYATEVPQPMVNL 181

Qy 162 MCMTGDLDTKASVFFKTNADGNTTCAKEMTKLSGISIIPMEICDFDFPCGYSMNAIH 221
Db 182 MCMTGDLDTKASVFFKTHADGHVSCAKEMTKLSGISIIPMEVECDFDFPCGYSMNAIN 241

Qy 222 GSASFTHVTPEDGFSYASYEVNGLDATALSYGDLVKRLVLCGFGSFSVAVIFGGRQ 281
Db 242 GSASFTHVTPEDGFSYASYEVNGLDATALSYGDLVKRLVLCGFGSFSVAVIFGGRGH 301

Qy 282 AGTWKELGAEAYDCNNMVEQELPGGILLIYQSFCAEDAV--ASSPKSVLRCFDG-ENA 338
Db 302 AATWKKGLDAEAYDCNNMVEQELPGCGLLIYQSFCAEELAVSAGSPRVFHFENVESG 361

Qy 339 APPAKCKLANLVCLLEKDAIEEKDGVLD 366
Db 362 HPLVKEGKLANLLAWRAEESLEEGTGAL 390

RESULT 4
S68990
adenosylmethionine decarboxylase (EC 4.1.1.50) - Madagascar periwinkle
N;Alternate names: S-adenosyl-L-methionine decarboxylase proenzyme
C;Species: Catharanthus roseus (Madagascar periwinkle)
C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: S68990
R;Schroeder, G.; Schroeder, J.
Eur. J. Biochem. 228, 74-78, 1995
A;Title: cDNAs for S-adenosyl-L-methionine decarboxylase from Catharanthus roseus, hetero-
in the active enzyme, and a conserved region in the 5' mRNA leader.
A;Reference number: S68989; MUID:95188916; PMID:7883014
A;Accession: S68990
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-357 <SCH>
A;Cross-references: UNIPROT:Q42679; EMBL:U12573; NID:g758693; PID:g758695
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;71/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match      44.6%; Score 854.5; DB 2; Length 357;
Best Local Similarity 47.6%; Pred. No. 4e-63;
Matches 185; Conservative 52; Mismatches 83; Indels 69; Gaps 8;

Qy 9 APPASAI GFEGYKRLIETFSAPVFDVPHGSGLRALSRSQIDSVLDLAR----- 58
Db 2 ALPASAI GFEGYKRLIETFSAPVFDVPHGSGLRALSRSQIDSVLDLARCTIVSELSNQ 61

Qy 59 -----KIVIKTCGTTKLLLTTPRILELAELSMPPLAAVKYRGRTIFFP 101
Db 62 YLDSYVLSSESLFVYPIKIIKTCGTTKLLLTTPRILELAELSMPPLAAVKYRGRTIFFP 121

Qy 102 GAOPAPHRFSSEVAVLNRYFGLKSGGNAYVIGDAARPGQKWHIYYATEVPEQ---PMV 158
Db 122 GAOPAPHRFSSEVAVLNRYFGLKSGGNAYVIGDPAKPGQKWHIYYATEVPEQ---PMV 180

Qy 159 NLEMCMTGLDITKASVFFKTNADGNTTCAKEMTKLSGISIIPMEICDFDFPCGYSMN 218
Db 181 TLEMCMTGLDITKASVFFKTSADGHTSCAKEMTKLSGISIIPMEICDFDFPCGYSMN 236
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submitted to the EMBL Data Library, November 1997
A:Reference number: Z14462
A:Accession: T01934
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-361 <PAR>
A:Cross-references: UNIPROT:Q04009; EMBL:AF031310; NID:G2687583; PID:G2687584
C:Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
K:Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F:/3/Modified site: pyruvic acid (Ser) (in mature form) $status predicted

      Query Match      43.8%; Score 837.5; DB 2; Length 361;
      Best Local Similarity 46.5%; Pred. No. 1e-61;
      Matches 182; Conservative 47; Mismatches 93; Indels 69; Gaps 8;

QY      9 APPASAIQFEGVEKRLKLETFSEAPVFDPHGSGGLAALSRQSDSVLDLAR----- 58
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      4 ALPVSIAIGFEGFEKRLKLEISFFEPFGLFADPNKGLSLSKAQLDETLGPAECTIVDSLND 63
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      59 -----KIVIKTCGTTKLLLTIPRILELAELSLMPLAAVKYSRGTFIFP 101
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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64	DVDSYVLSESSIFVYSYKIIITCGTTKLLIIPILKLAETLSLKQDVRVTRGSGFIP	123
	Db	
102	GAQPAPHRFSFEVAVLNRYFGGLKSGGNVYVIGDAAREPGQKWHIYATEYPEQ----	PMV 158
	QY	
124	GAQSPPHRFSEVAVLDGYFCKLAAGSKAVIMGSPDK-AQKWHVYSASAGPIQSNDPVY	182
	Db	
159	NLEMCWTGLDTWKASVFPKTNADGNTTCAKEMTKLSGISEIIPWEIICDFDFEPCGYSMN	218
	QY	
183	TLEMCWTGLDREKASVPYKTEG-----SSAAHMTVRSIGRIKILPNSGICDFEPEPCGYSMN	238
	Db	
219	ATHGSAFSTIHTVTPDDGFSYASYVWGLDATALSYGDLVKRVLGFCGSPSEFSVAVTIFGG	278
	QY	
239	STEGAAALSTIIHTPDDGFSYASFEAVGYDMTKVLGPLVERVLACFPQDFESIAL-----	293
	Db	
279	RQOAGTGWK-----ELGAEAYDCNNMVEQELPGGGIILYQSFCAABADVASSPKSVLRC	332
	QY	

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Db      294 --HADVATKLLERVSLDVKGYSLAEWSPEERFGKGSIVYQKF--TRTFPCGSPKSVLK- 348
QY      333 FDGENAAPPFAKCKLANLVLCLEEXDAIEKK 363
Db      349 -----GCKWEDEKEKE 361

RESULT 7
T06515
probable adenosylmethionine decarboxylase (EC 4.1.1.50) - garden pea
C:Species: Pisum sativum (garden pea)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06515
R:Carasco, P.; Marco, F.
submitted to the EMBL Data Library, June 1996
A:Description: Pea S-adenosylmethionine decarboxylase.
A:Reference number: Z15729
A:Accession: T06515
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-353 <CAR>
A:Cross-references: UNIPROT:Q43820; EMBL:U60592; NID:G1421750; PIDN:AA03865.1;
A:Experimental source: cv. Alaska
C:Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C:Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F:69/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

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Query Match      43.6%; Score 834; DB 2; Length 353;
Best Local Similarity 49.3%; P-red. No. 2e-61;
Matches 175; Conservative 52; Mismatches 90; Indels 38; Gaps 6;

Qy 13 SAIGPEGYKRLIEITFSEAPVFDHGSLRALSRQSDSVLD----- 55
Db 4 SAIGPEGFKRLIEIGFSDPLGFSDDQGRGLSRQSLQDDEIIAPAECTIVSSLANEDVD 63
Qy 56 -----LARKTVIKTCGTTKULLTTIPRILEAELMSPLAAVKYGRGTFIFFGAQP 105

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Db      64 YVLSSESLFVYAYKLIITCGTTKLLSIPILKLADISINVSRYTRGSFIFPGAQS 123
Qy      106 APHRSFSEEVAVLNRYFGGLKSGGNAYVIGDAARPGQKWHIYYATE--YPEQPMVNLEM 162
Db      124 FPHRFSEEVAVLDGFFGKLGSGSMAYILG-GSDEAQNWHIYCASSDSVSPGSGVYVYLEM 182
Qy      163 CMTGLDTKKASVPEKTNADGNTTCAKEMTKLSIGISEIIPMEICDFFPEPCGYSMAIHG 222
Db      183 CMTGLDREKASVFFKE-----QTGSAEMTNSGIRKILRNSEICDFFPEPCGYSMSNVEG 238
Qy      223 SAFSTIHTVPDGFSGSYASYEVMGLDATALSYGDLVKRVLCFGPSEFSVAVTIFGGRGOA 282
Db      239 SAVSTIHTVPDGFSGSYASFPETAGYDLKAINLNEMVRVLACFQTFESVAVHV-DNASKS 297
Qy      283 GTWKGELGAEAYDCNNMVQELPGGGILYIQSFCAAEADAVASGPKSVLRCFDCGEN 337
Db      298 FEQCLLDVKGVCCEKSHQGLGSGSVVYQKF--LKTSYCGSPRSTLKCWKDED 350

RESULT 8
Tl0707
adenosylmethionine decarboxylase (EC 4.1.1.50) 1 - clove pink
N;Alternate names: S-adenosylmethionine decarboxylase 1
C;Species: Dianthus caryophyllus (clove pink)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: Tl0707; Tl0787
R;Lee, M.M.; Lee, S.H.; Park, K.Y.
submitted to the EMBL Data Library, October 1995
A;Description: Nucleotide sequence of cDNAs encoding S-adenosylmethionine decarboxylase
A;Reference number: Z17089
A;Accession: Tl0707
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-381 <LEE>
A;Cross-references: UNIPROT:Q39676; EMBL:U38526; NID:g1155239; PID:g1155240
A;Experimental source: cv. White Sim; carnation petal
R;Kim, Y.J.; Lee, M.M.; Chang, K.S.; Lee, S.H.; Park, K.Y.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z17144
A;Accession: Tl0787
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-381 <KIM>
A;Cross-references: EMBL:U94786; NID:g2406584; PID:g2406585
A;Experimental source: strain White sim
C;Genetics:
A;Gene: gcsdc9
C;Function:
A;Description: catalyzes the decarboxylation of S-adenosyl-L-methionine to (5-deoxy-5-ade
C;Superfamily: polyamine biosynthesis
C;Keywords: blocked amino end; carbon-carbon lyase; eukaryotic type
F;93/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 43.1%; Score 825.5; DB 2; Length 381;
Best Local Similarity 48.3%; Pred. No. 1.1e-60;
Matches 180; Conservative 46; Mismatches 88; Indels 59; Gaps 8;

Qy      13 SAIGFEGYEKRLTTFSEAPFVDPHGSGLRALRSQIDSVLDLAR----- 58
Db      28 SAIGFEGEKRLEISFPFPGIFVDPEKGRLALSKAQLDILGPAECTIVDSLANSVDS 87
Qy      59 -----KIVIKTCGTTKLLITIPRILELAELSMPLAANKYSRGTFFPGAQP 105
Db      88 YVLSSESLFVYVSYKIIKTCGTTKLLHSILPILTLADGLCLDVKSVRYTRGSFIFPGAQS 147
Qy      106 APHRSFSEEVAVLNRYFGGLKSGGNAYVIGDAARPGQKWHIYYATEYP--EQPMVNLEM 163
Db      148 YPHRSFSEEVAVLDKYPFNGLTGSKAFVMSGPAKP-QKWHVYSATAPSDPDDPVYTLEM 206
Qy      164 MTGLDTKKASVPEKTNADGNTTCAKEMTKLSIGISEIIPMEICDFFPEPCGYSMAIHGS 223

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Db      207 MTGLDKGKASVFFKS---ESASAAVMVTSTGIRKILPDSALICDFFPEPCGYSMAIEGP 262
Qy      224 AFTIHTVPDGFSGSYASYEVMGLDATALSYGDLVKRVLCFGPSEFSVAVTI----- 275
Db      263 AVSTIHTVPDGFSGSYASFEAVGYDLKIVDNQVLVERVINCQPREFSIAVSDTADKYLE 322
Qy      276 -FGGRGOAGTWGELGAEAYDCNNMVQELPGGGILYIQSF--CAAEADAVASGPKSVLRC 332
Db      323 QYCAVNVAGYCRREGVEG-----LVGSGVLYIQKFGKATVUSGLNKSPK-----C 368
Qy      333 FDGENAAPFAKDC 345
Db      369 CRKEENDEKREC 381

RESULT 9
Tl0708
adenosylmethionine decarboxylase (EC 4.1.1.50) 2 - clove pink
N;Alternate names: S-adenosylmethionine decarboxylase 2
C;Species: Dianthus caryophyllus (clove pink)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: Tl0708
R;Lee, M.M.; Lee, S.H.; Park, K.Y.
submitted to the EMBL Data Library, October 1995
A;Description: Nucleotide sequence of cDNAs encoding S-adenosylmethionine decarboxylase
A;Reference number: Z17089
A;Accession: Tl0708
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-377 <LEE>
A;Cross-references: UNIPROT:Q39677; EMBL:U38527; NID:g1155241; PID:g1155242
A;Experimental source: cv. White Sim; carnation petal
C;Function:
A;Description: catalyzes the decarboxylation of S-adenosyl-L-methionine to (5-deoxy-5-ade
A;Pathway: polyamine biosynthesis
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;84/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 43.1%; Score 824.5; DB 2; Length 377;
Best Local Similarity 46.9%; Pred. No. 1.3e-60;
Matches 183; Conservative 46; Mismatches 90; Indels 71; Gaps 10;

Qy      13 SAIGFEGYEKRLTTFSEAPFVDPHGSGLRALRSQIDSVLDLAR----- 58
Db      19 SAIGFEGEKRLEISFPFPGIFVDPEKGRLALSKAHLDEILGPAECTIVDSLANSVDS 78
Qy      59 -----KIVIKTCGTTKLLITIPRILELAELSMPLAANKYSRGTFFPGAQP 105
Db      79 YVLSSESLFVYVSYKIIKTCGTTKLLNSIPILRLAETFLDVKSVRYTRGSFIFPGAQS 138
Qy      106 APHRSFSEEVAVLNRYFGGLKSGGNAYVIGDAARPGQKWHIYYATEYP--EQPMVNLEM 163
Db      139 FPHRSFSEEVAVLDNYFAKLGAGSKAIVMSGPKP-QKWHVYSATAPSDPDDPVYTLEM 197
Qy      164 MTGLDTKKASVPEKTNADGNTTCAKEMTKLSIGISEIIPMEICDFFPEPCGYSMAIHGS 223
Db      198 MTGLDREKASVFFKS---QSASAAVMVTSTGIRKILPDSVICDFFPEPCGYSMAIEGP 253
Qy      224 AFTIHTVPDGFSGSYASYEVMGLDATALSYGDLVKRVLCFGPSEFSVAVTIFGGRGOAG 283
Db      254 AVSTIHTVPDGFSGSYASFEAVGYDLQVVDLNLVLRVLACFEPKEFSIAV-----HADTD 308
Qy      284 TWKELGAEAYDCN-NMVE-----QELPGGGILYIQSFCAAEADAVA--SSPKSVLRUCF 333
Db      309 TADKVL---ARNGSVNVIGYSREBEGIEELGSGSVFYQKFCRGKATPVCPPAPKTKLC- 364
Qy      334 DGENAAPFAKDCCKLANLVLCLEEXDAIBEKD 363
Db      365 -----CWKEEIDEEME 376

RESULT 10

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S52662
adenosylmethionine decarboxylase (EC 4.1.1.50) TUB13 [similarity] - potato
A;Molecule type: mRNA
C;Species: Solanum tuberosum (potato)
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S52662; S28047
R;Arif, S.A.M.; Taylor, M.A.; George, L.A.; Butler, A.R.; Burch, L.R.; Davies, H.V.; Sta
Plant Mol. Biol. 26, 327-338, 1994
A;Title: Characterisation of the S-adenosylmethionine decarboxylase (SAMDC) gene of pota
A;Reference number: S52662; MUID: 95036004; PMID: 7948879
A;Accession: S52662
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-360 <ARI>
A;Cross-references: UNIPROT:Q04694; GB:S74514; NID:G807093; PIDN: AAB32507.1; PID:G807094
R;Taylor, M.A.; Arif, S.A.M.; Kumar, A.; Davies, H.V.; Scobie, L.A.; Pearce, S.R.; Flav
Plant Mol. Biol. 20, 641-651, 1992
A;Title: Expression and sequence analysis of cDNAs induced during the early stages of tu
A;Reference number: S28046; MUID: 93081725; PMID: 1450379
A;Accession: S28047
A;Molecule type: mRNA
A;Residues: 1-173, 'S', 175-256, 'T', 258-290, 'V', 292-304, 'I', 306-360 <TAY>
A;Cross-references: EMBL:Z11680; GB:S51455; NID:G21484; PIDN: CAA77742.1; PID:G21485
C;Genetics:
A;Gene: TUB13
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;73/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 43.0%; Score 822.5; DB 2; Length 360;
Best Local Similarity 48.5%; Pred. No. 1.8e-60;
Matches 176; Conservative 48; Mismatches 88; Indels 51; Gaps 8;
QY 11 PASAIGFEGEYKRLITFSEAPVFDVDPHGSLRALSRSQIDSVLDLAR----- 58
Db 6 PVSAGFEGEYKRLITFSEAPVFDVDPHGSLRALSRSQIDSVLDLAR----- 58
QY 59 -----KIVIKTCGTTKLLTTPRILELAELSMPAAVKYSGRTFFPGGA 103
Db 66 DSVLSESSLFVYPIKIIKTCGTTKLLTTPRILELAELSMPAAVKYSGRTFFPGGA 125
QY 104 QPAPHSFSEVAVLNRYFGLKSGGNAYVIGDAARPGQKHYYATEYPEQ-----PMVNL 160
Db 126 QSPFHRHSEVAVLDGFGKLAAGSAVINGSPDKT-QKHVYASAGVQSNDPYTL 184
QY 161 EMCWTGLDTRKASVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDPDFPEPCGYSNNAI 220
Db 185 EMCWTGLDTRKASVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDPDFPEPCGYSNNAI 240
QY 221 HGSAFSTIHTVPEDGFSYASVYVGLDATALSYGLVKRVLCGFGSPFSFSAVTFEGRG 280
Db 241 EGAAVSTIHTVPEDGFSYASVYVGLDATALSYGLVKRVLCGFGSPFSFSAVTFEGRG 293
QY 281 QAGTWGK-----ELGAEAYDCNNVQELPGGGLIYQSFCAEADAVASPKSVLR-QF 333
Db 294 HADVATKLLERTCSVDVKGYSLAEWSPEFEGGSIYVQKFP--TRTPCYCSPKSVLKGW 351
QY 334 DGE 336
Db 352 KEE 354

RESULT 11
T12613
adenosylmethionine decarboxylase (EC 4.1.1.50) - common sunflower
N;Alternate names: S-adenosylmethionine decarboxylase
C;Species: Helianthus annuus (common sunflower)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12613
R;Eliaeson, A.; Hamann, P.; Steinmetz, A.
submitted to the EMBL Data Library, May 1998
A;Description: Coding sequence for an S-adenosylmethionine decarboxylase from sunflower
A;Reference number: Z17552
A;Accession: T12613

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-361 <BLI>
C;Cross-references: UNIPROT:O65354; EMBL:AF066078; NID:G3153905; PID:G3153906
A;Experimental source: cultivar HA300; mature pollen
C;Genetics:
A;Gene: SAD
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;68/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 39.9%; Score 763.5; DB 2; Length 361;
Best Local Similarity 48.1%; Pred. No. 1.4e-55;
Matches 177; Conservative 49; Mismatches 87; Indels 55; Gaps 12;
QY 13 SAIGFEGEYKRLITFSEAPVFDVDPHGSLRALSRSQIDSVLDLAR----- 58
Db 3 SAIGFEGEYKRLITFSEAPVFDVDPHGSLRALSRSQIDSVLDLAR----- 58
QY 59 -----KIVIKTCGTTKLLTTPRILELAELSMPAAVKYSGRTFFPGGA 105
Db 63 YVLSSESLFVYPIKIIKTCGTTKLLTTPRILELAELSMPAAVKYSGRTFFPGGA 122
QY 106 APHRSFSEVAVLNRYFGLKSGGNAYVIGDAARPGQKHYYATEYPEQ-----PMVN 159
Db 123 FPHRSFSEVAVLNRYFGLKSGGNAYVIGDAARPGQKHYYATEYPEQ-----PMVN 181
QY 160 LEMCMTGLDTRKASVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDPDFPEPCGYSNNA 219
Db 182 LEMCMTGLDTRKASVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDPDFPEPCGYSNNA 237
QY 220 IHGSAFSTIHTVPEDGFSYASVYVGLDATALSYGLVKRVLCGFGSPFSFSAVTFEGGR 279
Db 238 IEGDAISTIHTVPEDGFSYASVYVGLDATALSYGLVKRVLCGFGSPFSFSAVTFEGGR 295
QY 280 QAGTWGKELGAEAYDCN-----NMVE-----QELPG-GGLIYQSFCAEADAVASPKSVL- 330
Db 296 NVV-----KOLNLENNVNVKGVNVEETKEVLGEGGSMVYVGF-ARGGSCGSPRSTLH 350
QY 331 RCF-DGEN 337
Db 351 RCF-DGEN 358

RESULT 12
T51378
adenosylmethionine decarboxylase (EC 4.1.1.50) [similarity] - Arabidopsis thaliana
N;Alternate names: protein FIN13_90
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: T51378
R;Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Ban
submitted to the Protein Sequence Database, August 2000
A;Reference number: Z25393
A;Accession: T51378
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-362 <SAT>
A;Cross-references: UNIPROT:Q9S779; EMBL:AL391145
A;Experimental source: cultivar Columbia; BAC clone FIN13
C;Genetics:
A;Map position: 5
A;Note: FIN13_90
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;68-69/Cleavage site: Glu-Ser (autolytic) #status predicted
F;69/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 39.6%; Score 757; DB 2; Length 362;
Best Local Similarity 45.6%; Pred. No. 4.9e-55;
Matches 170; Conservative 52; Mismatches 97; Indels 54; Gaps 9;
QY 13 SAIGFEGEYKRLITFSEAPVFDVDPHGSLRALSRSQIDSVLDLAR----- 58

```
Db 4 SAIGFEGYKRLVTFPEPGLFDLTQKGLRALAKSQIDELQPAECTIVSSLSNDQDS 63
Qy 59 -----KIVTKTCGTTKLLTIPRIELEABELSMPLAAVKYSGRTFFPGAQP 105
Db 64 YVLSSESLFFPYKIVIKVTCGTTKLLSIEPLRLAGELSLDKVAVYTRGSLFCGGQP 123
Qy 106 AHRSESEVAVLNRYFGGLKSGGNNAVIGDAARPGQKHYYIYATEYPEQPMVN---LEM 162
Db 124 FPHRNSEEVSLDGHFAKGLGSSVAYLMGDDDET-KKHVYVSASSANSNNKNVYVLEM 182
Qy 163 CMTGLDTPKASVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFDFPCGYSMAIHG 222
Db 183 CMTGLDKDASVYK-----NESSAGSMTDNGIRKILPQSOICDFEFPCGYSMSIEG 238
Qy 223 SAPSTIHTVPEDGFSVASYEVMGLDATALSYGDLVKRVLGCFGPSEFSVAV--TIFGGRG 280
Db 239 DAISTIHTVPEDGFSVASEAVGYDFTTMDLSHLVSKVLCFCFKPKQFSVAVHSTV---AQ 295
Qy 281 QAGTWGKELGAEAYDCNNMVEQEL-PGGGILIYQSF-----CAAEDAVASSPKSVLRCP 333
Db 296 KSYDGLSGLVDLDGCKESTMESLGEERGTVMYQRFKLGRYC-----GSPRSTLKCE 348
Qy 334 DGENAAPFAKDCK 346
Db 349 WSSNSCCNSEDEK 361

RESULT 13
T10750
probable adenosylmethionine decarboxylase (EC 4.1.1.50) - leaf mustard
C;Species: Brassica juncea (leaf mustard)
C;Date: 16-Jul-1999 #sequence revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10750
R;Lee, T.; Liu, J.J.; Pua, E.C.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z17116
A;Accession: T10750
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-369 <LEE>
A;Cross-references: UNIPROT:O49972; EMBL:U80916; NID:g2662405; PID:g2662406
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;69/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 39.2%; Score 751; DB 2; Length 369;
Best Local Similarity 46.1%; Pred. No. 1.6e-54;
Matches 167; Conservative 48; Mismatches 91; Indels 56; Gaps 9;

Qy 13 SAIGFEGYKRLVTFPEPGLFDLTQKGLRALAKSQIDSVLDLAR----- 58
Db 4 SAIGFEGYKRLVTFPEPGLFDLTQKGLRALAKSQIDSVLDLAR----- 63
Qy 59 -----KIVTKTCGTTKLLTIPRIELEABELSMPLAAVKYSGRTFFPGAQP 105
Db 64 YVLSSESLFFPYKIVIKVTCGTTKLLSIEPLRLAGELSLDKVAVYTRGSLFCGGQP 123
Qy 106 AHRSESEVAVLNRYFGGLKSGGNNAVIGDAARPGQKHYYIYATEYPEQPMVN----- 159
Db 124 FPHRNSEEVSLDGHFAKGLGSSVAYLMGDDDET-KKHVYVSASAPARNGNNNNVY 182
Qy 160 -LEMCTGLDTPKASVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFDFPCGYSMN 218
Db 183 TLEMCTGLDTPKASVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFDFPCGYSMN 238
Qy 219 AHRSESEVAVLNRYFGGLKSGGNNAVIGDAARPGQKHYYIYATEYPEQPMVN----- 278
Db 239 SVEGDAISTIHTVPEDGFSVASEAVGYDFTTMDLSHLVSKVLCFCFKPKQFSVAVHSSVA 298
Qy 279 RQAGTWGKELGAEAYDCNNMVEQELPG--GGILIYQSF-----CAAEDAVASSPKSVL 330
Db 299 QKSYDS-GLSVDLEDYGRE-TTIELLGEERGTVMYQRFKLGRYC-----GSPRSTL 349
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Qy 331 RC 332
Db 350 KC 351
```

RESULT 14

```
T22361
adenosylmethionine decarboxylase (EC 4.1.1.50) precursor [validated] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22361; T27363; T43626; T43521
R;White, S.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z19553
A;Accession: T22361
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-368 <WIL>
A;Cross-references: UNIPROT:O02655; EMBL:Z99171; PIDN:CAB16315.1; GSPDB:GN00019; CESP:F47G4.7
A;Experimental source: clone F47G4
submitted to the EMBL Data Library, June 1998
R;McLay, K.
A;Reference number: Z20356
A;Accession: T27363
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-368 <W12>
A;Cross-references: EMBL:AL023853; PIDN:CAA19560.1; GSPDB:GN00019; CESP:F47G4.7
A;Experimental source: clone Y71A12C
R;Da'dara, A.A.; Walter, R.D.
Biochem. J. 336, 545-550, 1998
A;Title: Molecular and biochemical characterization of S-adenosylmethionine decarboxylase
living nematode Caenorhabditis elegans, living nematode Caenorhabditis elegans.
A;Reference number: Z22535; MUID:99059682; PMID:9841864
A;Accession: T43626
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-368 <DAD>
A;Cross-references: EMBL:Y12499; PIDN:CAA73101.1
A;Accession: T43521
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-368 <DA2>
A;Cross-references: EMBL:Y12500; PIDN:CAA73102.1
C;Genetics:
A;Gene: samdc; F47G4.7
A;Map position: 1
A;Introns: 221/3; 294/2; 337/3
C;Function:
A;Description: EC 4.1.1.50 [validated, MUID:99059682]
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;83/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 19.7%; Score 377.5; DB 2; Length 368;
Best Local Similarity 32.3%; Pred. No. 1.5e-23;
Matches 108; Conservative 57; Mismatches 92; Indels 77; Gaps 16;

Qy 17 FEGYKRLVTFPEPGLFDLTQKGLRALAKSQIDSVLDLAR----- 58
Db 25 FEGAKLLLELWFCSS---TQNETSRIRIIPREIDAMDLDIARCKILKSHNESIDSVLS 81
Qy 59 -----KIVTKTCGTTKLLTIPRIELEABELS--MPLAAVKYSGRTFFPGAQP 107
Db 82 ESSLFISDNRNVLKTCGTTLLAALPVMQLAGAYAGLDQVQSVYYSRKNFLPDLQPSL 141
Qy 108 HRSFSEVAVLNRYFGGLKSGGNNAVIGDAARPGQKHYYIYATEYPEQPMVNLEM 162
Db 142 HKNFDAEYVLOSFF----VDGHAYCIGSLKQ--DRWLYTFHREFFFAHKQPDHTEI 195
Qy 163 CMTGLDTPKASVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFDFPCGYSMN 220
```

Db 196 LMSDLDEVLHKTQYAVDGNCFMR-----AGIDKIIIPAGADVHDELFDPCGYSMNAY 250
Qy 221 HGSA--PSTIHVTPEDGFSVASYEVWGLDATALSYGLV-----KRVLCGFGPSBSFSA 272
Db 251 MNDDQVATHVTPKAFSPSE-----TNQDLVCLYSQTRKVLQCFRPNK--IL 299
Qy 273 VTIFGGRGQAGTWGKELGAEAYDCNNMVEQLPG 306
Db 300 MTVFA--NDISEKGDQAQQQLWD-----RELPG 325

RESULT 15
DCHYDM
adenosylmethionine decarboxylase (EC 4.1.1.50) precursor - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: S22358; S19871
R:Tekwani, B.L.; Stanley, B.A.; Pegg, A.B.
Biochim. Biophys. Acta 1130, 221-223, 1992
A:Title: Nucleotide sequence of hamster S-adenosylmethionine decarboxylase cDNA.
A:Reference number: S22358; MUID:92223099; PMID:1562599
A:Accession: S22358
A:Molecule type: mRNA
A:Residues: 1-334 <TEK>
A:Cross-references: UNIPROT:P28918; EMBL:X63861; NID:G55521; PID:CAA45343.1; PID:G55522
A:Experimental source: liver of Syrian golden hamster
A:Note: the authors translated the codon ACA for residue 221 as Leu and AAG for residue 222 as Lys. The proenzyme is cleaved after translation into an alpha chain and a beta chain. The proenzyme is cleaved after translation into an alpha chain and a beta chain. The proenzyme is cleaved after translation into an alpha chain and a beta chain.
C:Comment: The proenzyme is cleaved after translation into an alpha chain and a beta chain. The proenzyme is cleaved after translation into an alpha chain and a beta chain. The proenzyme is cleaved after translation into an alpha chain and a beta chain.
C:Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C:Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase; polyamine biosynthesis
F:1-67/Domain: alpha chain #status predicted <CHA>
F:1-67/Domain: alpha chain #status predicted <CHA>
F:1-67/Domain: alpha chain #status predicted <CHA>
F:68-334/Domain: beta chain #status predicted <CHB>
F:68-334/Domain: beta chain #status predicted <CHB>
F:68/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 18.8%; Score 359.5; DB 1; Length 334;
Best Local Similarity 33.6%; Pred. No. 4e-22;
Matches 99; Conservative 45; Mismatches 100; Indels 51; Gaps 12;

Qy 17 FEYERKLEITPSEAPVFPVDPHGSLRALRSQID-----SVLDLA----- 57
Db 7 FEGETKLELVFWSRQSDASQSGSGLRTIPRSEWDVLLKDVQCIIISVTKTQKQAYVLS 66
Qy 58 -----RKIVIKTCGTTKLLTIPRIELABELS--MPLAAVKYSRGTFIPGQAPAP 107
Db 67 ESSMFVSKRPFILKTCGTTLLKALVPLKLARDYSGFDSIQSFYFSRKNFMKPSHQGP 126
Qy 108 HRSFSBEVAVLNRYFGGLKSGGNAYVIGDAAPQKWHIYYATEYPEQPMVN-----LEM 162
Db 127 HRNFQEEIEFLNAIF---PNGAAYCNG--RMNSDCWYL-YTLDFPESRVINQPDQTL 179
Qy 163 CMTGLDTKASVFKTNADGNTTCAKEMTKLGISETIIPMEICDFDFPCGYSMNAIHG 222
Db 180 LMSLDPAVMDQFYM--KDGVT--AKDVTRESGIRDLIPGSVIDATLFPNCGYSMNGMKS 235
Qy 223 -SAFSTHVTPEGFSVASYEVWGLDATALSYGLVLCGFCGSPSEFSVAVTIF 276
Db 236 DGTWTIHTPEPEFSYVSPET---NLQSYYDILIRKVVVEFKPGKF--VTTLF 285

Search completed: May 11, 2005, 22:59:06
Job time : 21.6014 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2005, 22:40:28 ; Search time 75.8763 Seconds
(without alignments)
1620.151 Million cell updates/sec

Title: US-10-732-923-407

Perfect score: 1914

Sequence: 1 MAVLSAAGAPPAISAIGFEGY.....NLVCLFEAIBKDGVLDE 368

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 1432185

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1853	96.8	366	15	US-10-310-154-457
2	1746.5	91.2	397	16	US-10-767-701-47033
3	1726	90.2	400	15	US-10-310-154-458
4	1538	80.4	450	16	US-10-437-963-147033
5	1538	80.4	466	16	US-10-437-963-147475
6	1458	76.2	395	16	US-10-437-963-142922
7	1458	76.2	554	16	US-10-437-963-142921
8	1439.5	75.2	305	15	US-10-425-114-39365
9	1393	72.8	398	16	US-10-767-701-46359
10	1365.5	71.4	289	15	US-10-425-114-56960
11	1365.5	71.3	416	15	US-10-425-114-57997
12	1365.5	71.3	416	15	US-10-425-114-67343
13	1359.5	71.0	422	15	US-10-425-114-36776

14	1302.5	68.1	276	15	US-10-425-114-69727	Sequence 69727, A
15	1244	65.0	392	16	US-10-437-963-128930	Sequence 128930, A
16	1218.5	63.7	395	16	US-10-767-701-46141	Sequence 46141, A
17	842.5	44.0	187	15	US-10-425-114-57416	Sequence 57416, A
18	829	43.3	355	15	US-10-424-599-249854	Sequence 249854, A
19	829	43.3	355	15	US-10-424-599-249859	Sequence 249859, A
20	829	43.3	356	15	US-10-425-114-46255	Sequence 46255, A
21	829	43.3	356	15	US-10-425-114-46648	Sequence 46648, A
22	809	42.3	355	15	US-10-424-599-249855	Sequence 249855, A
23	809	42.3	355	15	US-10-424-599-249858	Sequence 249858, A
24	809	42.3	360	15	US-10-425-114-43048	Sequence 43048, A
25	809	42.3	360	15	US-10-425-114-4323	Sequence 46323, A
26	802	41.9	363	14	US-10-425-114-47297	Sequence 47297, A
27	799.5	41.8	181	15	US-10-425-114-57901	Sequence 57901, A
28	778.5	40.7	173	15	US-10-425-114-56901	Sequence 56901, A
29	768	40.1	361	15	US-10-424-599-205003	Sequence 205003, A
30	751	39.2	331	15	US-10-425-114-71868	Sequence 71868, A
31	686	35.8	203	15	US-10-425-114-58490	Sequence 58490, A
32	676.5	35.3	156	15	US-10-425-114-47572	Sequence 47572, A
33	546.5	28.6	224	15	US-10-424-599-205002	Sequence 205002, A
34	468	24.5	359	16	US-10-437-963-166485	Sequence 166485, A
35	456.5	23.9	113	15	US-10-425-114-56995	Sequence 56995, A
36	439.5	23.0	216	15	US-10-425-114-45581	Sequence 45581, A
37	377.5	19.7	368	15	US-10-369-493-5296	Sequence 5296, Ap
38	377.5	19.7	368	15	US-10-369-493-5297	Sequence 5297, Ap
39	360.5	18.8	348	9	US-09-925-300-1167	Sequence 1167, Ap
40	356.5	18.6	334	15	US-10-341-434-12	Sequence 12, Appl
41	356.5	18.6	334	15	US-10-341-434-20	Sequence 20, Appl
42	356.5	18.6	334	15	US-10-341-434-127	Sequence 127, Appl
43	356.5	18.6	334	17	US-10-753-267-50	Sequence 50, Appl
44	346	18.1	369	15	US-10-369-493-2553	Sequence 2553, Ap
45	334	17.5	478	15	US-10-436-327-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-10-310-154-457
; Sequence 457, Application US/10310154
; Publication No. US2003023670A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Chomet, Paul S.
; APPLICANT: Adams, Thomas H
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Agarwal, Ameeta K.
; APPLICANT: Ahrens, Jeffrey E.
; APPLICANT: Ball, James A.
; APPLICANT: Banu, G.
; APPLICANT: Bell, Erin
; APPLICANT: Boddupalli, Raghava
; APPLICANT: Deikman, Jill
; APPLICANT: Deng, Molian
; APPLICANT: Dong, Jinzhao
; APPLICANT: Duff, Stephen M.
; APPLICANT: Galligan, Meghan M.
; APPLICANT: Hinchey, Brenda S.
; APPLICANT: Huang, Shihshieh
; APPLICANT: Johnson, G. Richard
; APPLICANT: Jung, Vincent
; APPLICANT: Kretzmer, Keith A
; APPLICANT: Laccetti, Lucille B.
; APPLICANT: Lai, Chao-Qiang
; APPLICANT: Lee, Gary
; APPLICANT: Lin, Jie-Yi
; APPLICANT: Liu, Jingdong
; APPLICANT: Lu, Bin
; APPLICANT: Luethy, Michael M.
; APPLICANT: Lund, Adrian
; APPLICANT: Madson, Linda L.
; APPLICANT: Malloy, Kathleen A.
; APPLICANT: McKiel, Christine L.

APPLICANT: McKiel, Christine L.
APPLICANT: Miller, Philip W.
APPLICANT: Padmavathi, Manchikanti
APPLICANT: Parnell, Laurence D.
APPLICANT: Start, William G.
APPLICANT: Tennessee, Dan
APPLICANT: Vidya, K.R.
APPLICANT: Wang, Haiyun
APPLICANT: Xin, Zhanqun
APPLICANT: Xu, Nanfei
APPLICANT: Yang, Chunzhi
APPLICANT: Zeng, Xiaoping
APPLICANT: Zhang, Qiang
APPLICANT: Zhao, Yajuan
APPLICANT: Zhou, Li
TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
FILE REFERENCE: 38-15(52796)B
CURRENT APPLICATION NUMBER: US/10/310,154
PRIOR FILING DATE: 2002-12-04
CURRENT FILING DATE: 2002-12-04
PRIOR FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 736
SEQ ID NO 458
LENGTH: 400
TYPE: PRT
ORGANISM: Zea mays
US-10-310-154-458

Query Match 90.2%; Score 1726; DB 15; Length 400;
Best Local Similarity 84.5%; Pred. No. 2.2e-173;
Matches 338; Conservative 8; Mismatches 22; Indels 32; Gaps 3;
QY 1 MAVLSAAGAPPASAIAGFEGYKRLTTFSEAPVFPVDPHGSLRALSRQSDVLDLAR-- 58
DB 1 MAVLSAADASPVSAIGFEGYKRLTTFSEAPVFPVDPHGSLRALSRQSDVLDLARCT 60
QY 59 -----KIVIKTCGTTKLLLTIPRIELAEELSMPLAAYKY 93
DB 61 IVSELNKPDSYVLSSESLFIYPLKIVIKTCGTTKLLLTIPRIELAEELSMPLAAYKY 120
QY 94 SRGTFTPPGAQAPHRSPSEAVLNRYFGGLKSGGNAYVIGDAPRGQKWHIYYATEYP 153
DB 121 SRGTFTPPGAQAPHRSPSEAVLNRYFGGLKSGGNAYVIGDAPRGQKWHIYYATEYP 180
QY 154 EQPMVNLWCMTGLDTKASVFPKTNADGNNTTCAKEMTKLSGISEIIPEMEICDFDFEPC 213
DB 181 EQPMVNLWCMTGLDKKACVFPKTNADGNNTTCAKEMTKLSGISEIIPEMEICDFDFEPC 240
QY 214 GYSMAIHGSAFSTIHVTPEDGFSYASYEVWGLDATALSYGDLVKRVLGCGFSPSEFSVAV 273
DB 241 GYSMAIHGSAFSTIHVTPEDGFSYASYEVWGLDATALSYGDLVKRVLGCGFSPSEFSVAV 300
QY 274 TIFGGGQAGTWKELGAAYDCNNMVEQBLPGGGLIYQSFCAAEADAVASSPKSVLRCP 333
DB 301 TIFGGGAGTGWKALGAAYDCNNMVEQBLPGGGLIYQSFCAAEADAVATSPKSVFHC 360
QY 334 DGENA----APFACKCLANVCL-BEXDAIEEKDGVLD 368
DB 361 DGENVSAPPMPKDYKLANLLCWEEADAMEKAGVLD 400

RESULT 4
US-10-437-963-147033
Sequence 147033, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 147033
LENGTH: 450
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT MRT4530_475C.1.pcp
US-10-437-963-147033

Query Match 80.4%; Score 1538; DB 16; Length 450;
Best Local Similarity 77.0%; Pred. No. 2.1e-150;
Matches 308; Conservative 18; Mismatches 43; Indels 34; Gaps 5;
QY 1 MAVLSAAGAPPASAIAGFEGYKRLTTFSEAPVFPVDPHGSLRALSRQSDVLDLAR-- 58
DB 53 MGVLSSAADPPVSAIGFEGYKRLTTFSEAPVFPVDPHGSLRALSRQSDVLDLARCT 112
QY 59 -----KIVIKTCGTTKLLLTIPRIELAEELSMPLAAYKY 93
DB 113 IVSELNKPDSYVLSSESLFIYSDKIVIKTCGTTKLLLTIPRIELAEELSMPLAAYKY 172
QY 94 SRGTFTPPGAQAPHRSPSEAVLNRYFGGLKSGGNAYVIGDAPRGQKWHIYYATEYP 153
DB 173 SRGMFIFPSAQAAPHRSPSEAVLNRYFGHLKSGGNAYVIGDAPRGQKWHIYYATQHP 232
QY 154 EQPMVNLWCMTGLDTKASVFPKTNADGNNTTCAKEMTKLSGISEIIPEMEICDFDFEPC 213
DB 233 EQPMVNLWCMTGLDKKASVFPKTSADGHTSACAKEMTKLSGISDIIPEMEICDFDFEPC 292
QY 214 GYSMAIHGSAFSTIHVTPEDGFSYASYEVWGLDATALSYGDLVKRVLGCGFSPSEFSVAV 273
DB 293 GYSMAIHGSAFSTIHVTPEDGFSYASYEVWGLDATALSYGDLVKRVLGCGFSPSEFSVAV 352
QY 274 TIFGGGQAGTWKELGAAYDCNNMVEQBLPGGGLIYQSFCAAEADAVASSPKSVLR 331
DB 353 TIFGGGAGTGWKALGAAYDCNNMVEQBLPGGGLIYQSFCAAEADAVATSPKSVLH 412
QY 332 CFDEG---NAAFPACKCLANVCLBEXDAIEEKDGVLD 368
DB 413 CFDAENWNPAP-VKSGKLGNNLLPWGE-DALENDGVFDE 450

RESULT 5
US-10-437-963-147475
Sequence 147475, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 147475
LENGTH: 466
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure

```

; LOCATION: (1)...(466)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_479C.1.pep
US-10-437-963-147475

Query Match      80.4%; Score 1538; DB 16; Length 466;
Best Local Similarity 77.0%; Pred. No. 2.2e-153;
Matches 308; Conservative 18; Mismatches 40; Indels 34; Gaps 5;

QY 1 MAVLSAAGAPPASAI GFE GYKLEITFS EAPVFPVDPHGSLRALSRQSDSVLDLAR-- 58
Db 69 MGVLSAADPPVSAI GFE GYKLEITFS EAPVFPVDPHGSLRALSRQSDSVLDLARCT 128
QY 59 -----KIVIKTCGTTKLLLTIPRILELAELSPLAAVKY 93
Db 129 IVSELSNEVPDSYVLSSESLFYSDKIVIKTCGTTKLLLTIPRILELAELSPLAAVKY 188
QY 94 SRTGTFPPGAOPAPHRSFSEEVAVLNRYFGGLSGGNAYVIGDAARPGQKWHIYYATEYP 153
Db 189 SRGMFI PPSAOPAPHRSFSEEVAVLNRYFGHLKSGGNAYVIGDPAKPGQKWHIYYATQHP 248
QY 154 EQPMVNLMECMTGLDTKASVFFKTNADGNNTTCAKEMTKLSGISEIIPEMEICDFDFEPC 213
Db 249 EQPMVNLMECMTGLDKKASVFFKTSADGHTTCAKEMTKLSGSDIIPEMEICDFDFEPC 308
QY 214 GYSNNAIHGSAFTIHTVPEDGFSYASYEVMGLDATALSYGDLVKRVLCFGSPSEFSVAV 273
Db 309 GYSNNAIHGSAFTIHTVPEDGFSYASYEVMGLDATALSYGDLVKRVLCFGSPSEFSVAV 368
QY 274 TIFGGGGOAGTWCKELGAEAYDCNNMVQELPGGGLIYQSFCAED--AVASSPKSVLR 331
Db 369 TIFGGHGHAGTWAKELNADAYCNNMVQELPGGGLIYQSFDTATEDVPVAVGSPKSVLH 428
QY 332 CFPGGE---NNAAPFAKCKLANLVCLBEXDAIEEKDGVLDE 368
Db 429 CFEAENWNPAP-VKSGKLGNLPLWGBE-DALENDGVFDE 466

RESULT 6
US-10-437-963-142922
; Sequence 142922, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 142922
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_43881C.1.pep
US-10-437-963-142922

Query Match      76.2%; Score 1458; DB 16; Length 395;
Best Local Similarity 73.0%; Pred. No. 4.9e-145;
Matches 286; Conservative 25; Mismatches 47; Indels 34; Gaps 3;

QY 1 MAVLSAAGAPPASAI GFE GYKLEITFS EAPVFPVDPHGSLRALSRQSDSVLDLAR-- 58
Db 1 MAVLSVADSPVPSAI GFE GYKLEITFS EAPVFPVDPHGSLRALSRQSDSVLDLARCT 60

RESULT 7
US-10-437-963-142921
; Sequence 142921, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 142921
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_43880C.1.pep
US-10-437-963-142921

Query Match      76.2%; Score 1458; DB 16; Length 554;
Best Local Similarity 73.0%; Pred. No. 8.2e-145;
Matches 286; Conservative 25; Mismatches 47; Indels 34; Gaps 3;

QY 1 MAVLSAAGAPPASAI GFE GYKLEITFS EAPVFPVDPHGSLRALSRQSDSVLDLAR-- 58
Db 72 MAVLSVADSPVPSAI GFE GYKLEITFS EAPVFPVDPHGSLRALSRQSDSVLDLARCT 131
QY 59 -----KIVIKTCGTTKLLLTIPRILELAELSPLAAVKY 93
Db 132 IVSELSNEVPDSYVLSSESLFYSDKIVIKTCGTTKLLLTIPRILELAELSPLAAVKY 191
QY 94 SRTGTFPPGAOPAPHRSFSEEVAVLNRYFGGLSGGNAYVIGDAARPGQKWHIYYATEYP 153
Db 192 SRTGTFPPGAOPAPHRSFSEEVAVLNRYFGGLSGGNAYVIGDPAKPGQKWHIYYATQHP 251
QY 154 EQPMVNLMECMTGLDTKASVFFKTNADGNNTTCAKEMTKLSGISEIIPEMEICDFDFEPC 213
Db 252 EQPMVNLMECMTGLDKKASVFFKTSADGHTTCAKEMTKLSGSDIIPEMEICDFDFEPC 311

```

Qy 214 GYSNNAIHGSAFSTIHTVPEDGFSYASYEVNGLDATALSYGDLVKRVLCGFGPSEFSVAV 273
Db 312 GYSNNAIHGSAFSTIHTVPEDGFSYASYEVNGLDATALSYGDLVKRVLCGFGPSEFSVAV 371
Qy 274 TIFGRCQAGTWKELGAEAYDCNNMVEOELPGGILLIYQSFCAEDAVASSPKSVLCRF 333
Db 372 TIFGRRHAGTWAGLDVGAYSCNNMVEOELPGGILLIYQSFATATBIATGSPRSVLHCF 431
Qy 334 DGENAAPFAKCKLANIIVCLE-EXDAIEEKDG 364
Db 432 ADENTE-----KAGKMEALYWEDDAVEIDG 457

RESULT 8
US-10-425-114-39365
; Sequence 39365, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 39365
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700074853_FLI.pep
US-10-425-114-39365

Query Match 75.2%; Score 1439.5; DB 15; Length 305;
Best Local Similarity 90.2%; Pred. No. 3e-143;
Matches 275; Conservative 7; Mismatches 18; Indels 5; Gaps 2;

Qy 69 KLLTTPRIELEABELSMPLAAVKYSGTTFIPGAQAPAPHRSPSEEVAVLNRYFGGLKSG 128
Db 1 KLLTTPRIELEABELSMPLAAVKYSGTTFIPGAQAPAPHRSPSEEVAVLNRYFGGLKSG 60

Qy 129 GNAYVIGDAPRGQKWHIYYATEYPEQPMVNLEMCMTGLDTKKASVFFKTNADGNTTCAK 188
Db 61 GNAYVIGDAPRGQKWHIYYATEYPEQPMVNLEMCMTGLDTKKASVFFKTNADGNTTCAK 120

Qy 189 EMTKLSGISIIPEMEICDFDFPCGYSMNAIHGSAFSTIHTVPEDGFSYASYEVNGLDA 248
Db 121 EMTKLSGISIIPEMEICDFDFPCGYSMNAIHGSAFSTIHTVPEDGFSYASYEVNGLDA 180

Qy 249 TALSYGDLVKRVLCGFGPSEFSVAVTIFGRCQAGTWKELGAEAYDCNNMVEOELPGGG 308
Db 181 TALSYGDLVKRVLCGFGPSEFSVAVTIFGRCQAGTWKELGAEAYDCNNMVEOELPGGG 240

Qy 309 ILIYQSFCAEDAVASSPKSVLCRFDENA-----APFAKCKLANIIVCL-EEKDAIEEKD 363
Db 241 LLYYQSFCAEDAVATSPKSVFHFCDGENVESAPPPMKDYKLANILLCWEEDAMEKA 300

Qy 364 GVLDE 368
Db 301 GVLDE 305

RESULT 9
US-10-767-701-46359
; Sequence 46359, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 46359
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C1511_1.pep
US-10-767-701-46359

Query Match 72.8%; Score 1393; DB 16; Length 398;
Best Local Similarity 70.4%; Pred. No. 3.8e-138;
Matches 276; Conservative 35; Mismatches 49; Indels 32; Gaps 4;

Qy 1 MAVL--SAAGAPPASAIPEGYEKRLIETFEAPVFDPHGSLRLALSRQIDSVLDLAR 58
Db 1 MAVLQVAAAAPPVPSAIGFEGYEKRLIETFEAPVFDPHGSLRLALSRQIDSVLDLAR 60

Qy 59 -----KIVIKTCGTTKLLLTIPRIELEABELSMPLAAV 91
Db 61 CTIVSLSLNEFDSDYVLSASSLFVYPMVKIKTCGTTKLLLTIPRIELEABELSMPLAAV 120

Qy 92 KYSGTTFIPGAQAPAPHRSPSEEVAVLNRYFGGLKSGNAYVIGDAARPGQKWHIYYATE 151
Db 121 KYSGTTFIPGAQAPAPHRSPSEEVAVLNRYFGGLKSGNAYVIGDAARPGQKWHIYYATE 180

Qy 152 YPEQPMVNLEMCMTGLDTKKASVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDFDFE 211
Db 181 HPEEPVVTLEMCMTGLDKKASVFFKTSADGYTSCAKEMTKLSGISIIPEMEICDFDFE 240

Qy 212 PCGYSMNAIHGSAFSTIHTVPEDGFSYASYEVNGLDATALSYGDLVKRVLCGFGPSEFSV 271
Db 241 PCGYSMNAIHGSAFSTIHTVPEDGFSYASYEVNGLDATALSYGDLVKRVLCGFGPSEFSV 300

Qy 272 AVTIFGRCQAGTWKELGAEAYDCNNMVEOELPGGILLIYQSFCAEDAVASSPKSVLR 331
Db 301 AVTIFGRCQAGTWKELGAEAYDCNNMVEOELPGGILLIYQSFCAEDAVASSPKSVLR 360

Qy 332 CPDGENAAPFAKCKLANIIVCLE-EEKDAIEEKD 363
Db 361 DFAGDIVKP--GDSGEADGFCW-EADAVDESE 389

RESULT 10
US-10-425-114-56960
; Sequence 56960, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 56960
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17089E06_FLI.pep
US-10-425-114-56960


```
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53113)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 36776
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB136-020-E2_FLI.pep
US-10-425-114-36776

Query Match          71.0%; Score 1359.5; DB 15; Length 422;
Best Local Similarity 67.4%; Pred. No. 1.4e-134;
Matches 269; Conservative 33; Mismatches 48; Indels 49; Gaps 4;

QY 1 MAVL--SAAGAPPASAIAGFEGYKRLITPSEAPVFDVPHGSLRALRSQIDSVLDLAR 58
DB 28 MAVLVQAAAAPPVSVVIGFEGPEKRLISFSEAPVLADPSGRGLRALSRAQIDSVLDLAR 87
QY 59 -----KIVIKTCGTTKLLTIPRILELAELSMLAAV 91
DB 88 CTIVSELNEDFDSYVLSSESLFVYPVKIVIKTCGTTKLLTIPRILELAELSMLAAV 147
QY 92 KYSGTFIFPGAQAPAPHRSESEAVLNRYFGLKSGGNAYVIGDAARPGOKWHIYYATE 151
DB 148 KYSGTFIFPGAQAPAPHRSESEAVLNRYFGLKSGGNAYVIGDAARPGOKWHIYYAE 207
QY 152 YPQPQVNMCMGTGLDTKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDE 211
DB 208 HPEPVVTEMCMGTGLDKKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDE 267
QY 212 PCYSNNAIHGSAPSTIHTVTPEDGFSYASVYVMDLATALSYGDLVKRVLCGFGPSEFSV 271
DB 268 PCYSNNAHVGPALSTIHTVTPEDGFSYASVYVMDLATALSYGDLVKRVLCGFGPSEFSV 327
QY 272 AVTIFGRCGAGTWKELGAEYDCNNMVEQELPGGILLIYQSFCAEDAVASSPKSVLR 331
DB 328 AVTIFGRCGAGTWKELGAEYDCNNMVEQELPGGILLIYQSFCAEDAVASSPKSVLR 387
QY 332 CPDG-----ENAAPFAKCKLANLVCLLEEXDAIEBKD 363
DB 388 DFAGDIVKRNSESDAPW-----EADAVDESE 413

RESULT 14
US-10-425-114-69727
; Sequence 69727, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53113)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 69727
; LENGTH: 276

; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17199H04_FLI.pep
US-10-425-114-69727

Query Match          68.1%; Score 1302.5; DB 15; Length 276;
Best Local Similarity 89.1%; Pred. No. 8.2e-129;
Matches 246; Conservative 7; Mismatches 18; Indels 5; Gaps 2;

QY 98 FIFPGAQAPAPHRSESEAVLNRYFGLKSGGNAYVIGDAARPGOKWHIYYATEYEQPM 157
DB 1 FIFPGAQAPAPHRSESEAVLNRYFGLKSGGNAYVIGDAARPGOKWHIYYATEYEQPM 60
QY 158 VNLEMCMTGLDTKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDEPFCGYSM 217
DB 61 VNLEMCMTGLDKKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDEPFCGYSM 120
QY 218 NAIHGSAPSTIHTVTPEDGFSYASVYVMDLATALSYGDLVKRVLCGFGPSEFSVAVTIFG 277
DB 121 NAIHGSAPSTIHTVTPEDGFSYASVYVMDLATALSYGDLVKRVLCGFGPSEFSVAVTIFG 180
QY 278 GRGQAGTWKELGAEYDCNNMVEQELPGGILLIYQSFCAEDAVASSPKSVLCRFDGEN 337
DB 181 GRGAGTWKALGAEYDCNNMVEQELPGGILLIYQSFCAEDAVASSPKSVLCRFDGEN 240
QY 338 A----APPAKCKLANLVCL-BEXDAIEBKDGVLDE 368
DB 241 VESAPPMKKDYKLANLLCWEEDAMBEKAGVLDE 276

RESULT 15
US-10-437-963-128930
; Sequence 128930, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 128930
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_31236C.1.pep
US-10-437-963-128930

Query Match          65.0%; Score 1244; DB 16; Length 392;
Best Local Similarity 62.6%; Pred. No. 2.1e-122;
Matches 244; Conservative 48; Mismatches 68; Indels 30; Gaps 3;

QY 1 MAVLSAAGAPPASAIAGFEGYKRLITPSEAPVFDVPHGSLRALRSQIDSVLDLAR-- 58
DB 3 MSLADWSAGSAPASPIGFEYKRLITLSDAPVFDVPCGRGLRALREQIDSLDLAKCT 62
QY 59 -----KIVIKTCGTTKLLTIPRILELAELSMLAAVKY 93
DB 63 IVSHLSNKHFDSDVLSSESLFVYPVKVLTCTGTTKLLTIPRILELAELSMLAAVKY 122
QY 94 SRGTFFPGAQAPAPHRSESEAVLNRYFGLKSGGNAYVIGDAARPGOKWHIYYATEYP 153
DB 123 SRGMFIFPGAQAPAPHRSESEAVLNRYFGLKSGGNAYVIGDAARPGOKWHIYYATEYP 182
```

```
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53113)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 36776
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB136-020-E2_FLI.pep
US-10-425-114-36776

Query Match          71.0%; Score 1359.5; DB 15; Length 422;
Best Local Similarity 67.4%; Pred. No. 1.4e-134;
Matches 269; Conservative 33; Mismatches 48; Indels 49; Gaps 4;

QY 1 MAVL--SAAGAPPASAIAGFEGYKRLITPSEAPVFDVPHGSLRALRSQIDSVLDLAR 58
DB 28 MAVLVQAAAAPPVSVVIGFEGPEKRLISFSEAPVLADPSGRGLRALSRAQIDSVLDLAR 87
QY 59 -----KIVIKTCGTTKLLTIPRILELAELSMLAAV 91
DB 88 CTIVSELNEDFDSYVLSSESLFVYPVKIVIKTCGTTKLLTIPRILELAELSMLAAV 147
QY 92 KYSGTFIFPGAQAPAPHRSESEAVLNRYFGLKSGGNAYVIGDAARPGOKWHIYYATE 151
DB 148 KYSGTFIFPGAQAPAPHRSESEAVLNRYFGLKSGGNAYVIGDAARPGOKWHIYYAE 207
QY 152 YPQPQVNMCMGTGLDTKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDE 211
DB 208 HPEPVVTEMCMGTGLDKKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDE 267
QY 212 PCYSNNAIHGSAPSTIHTVTPEDGFSYASVYVMDLATALSYGDLVKRVLCGFGPSEFSV 271
DB 268 PCYSNNAHVGPALSTIHTVTPEDGFSYASVYVMDLATALSYGDLVKRVLCGFGPSEFSV 327
QY 272 AVTIFGRCGAGTWKELGAEYDCNNMVEQELPGGILLIYQSFCAEDAVASSPKSVLR 331
DB 328 AVTIFGRCGAGTWKELGAEYDCNNMVEQELPGGILLIYQSFCAEDAVASSPKSVLR 387
QY 332 CPDG-----ENAAPFAKCKLANLVCLLEEXDAIEBKD 363
DB 388 DFAGDIVKRNSESDAPW-----EADAVDESE 413

RESULT 14
US-10-425-114-69727
; Sequence 69727, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53113)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 69727
; LENGTH: 276
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Qy	154	EQPMVLEMCMTGLDTKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFPC	213
Db	183	EQPMVTLEMCMTGLDAKAEVFFKSDTSGSCSAKEMTFSGISEIIPEMEICDFDFPC	242
Qy	214	GYSMNAIHGSAFSTIHVTPEDGFSYASYEVNGLDATALSYGDLVKRVLGCFGPSEFSVAV	273
Db	243	GYSMNGIYGPAVSTIHVTPPEGFSYASYEAMNFPSSLVYDDLIKKVLACFCPSDFSVA	302
Qy	274	TIFGGRQAGTWKELGAAYDCNNMVEQLPGGGLIYQSFCAAEADAVASSPKSVLRCF	333
Db	303	TIFGHHGFAKSWAKAEVDSYMCDDLVEQLPGGVLMYQSFTAVTPG-AVSPRSTLDGW	361
Qy	334	DGENAAPPFAKCKLANLVCLLEEXDAEEKD	363
Db	362	NSDGAEMVAKSEMS--VCWEGEKAAKKKD	389

Search completed: May 11, 2005, 22:57:57
Job time : 76.8763 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2005, 22:39:42 ; Search time 24.3436 Seconds
(without alignments)
1128.461 Million cell updates/sec

Title: US-10-732-923-407
Perfect score: 1914
Sequence: 1 MAVLSAAGAPPASAIAGFEY.....NLVLEEXDAIBEKGVLD 368

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pap.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pap.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pap.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pap.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pap.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	360.5	18.8	348	4	US-09-949-016-10038
2	356.5	18.6	334	4	US-09-917-254-54
3	331	17.3	424	4	US-09-248-796A-18169
4	97.5	5.1	350	4	US-09-302-540-11867
5	96.5	5.0	410	4	US-09-010-877-2
6	94.5	4.9	331	4	US-09-710-279-874
7	94.5	4.9	331	4	US-09-710-279-2244
8	94.5	4.9	342	3	US-09-134-001C-5198
9	94.5	4.9	634	4	US-09-248-796A-19513
10	89	4.6	308	3	US-09-189-060B-70
11	89	4.6	3546	4	US-09-679-279-13
12	86.5	4.5	355	1	US-08-008-688A-2
13	86.5	4.5	545	4	US-09-604-957-4
14	86.5	4.5	1430	3	US-09-008-172-2
15	86.5	4.5	1430	3	US-09-210-361-6
16	86.5	4.5	1430	4	US-09-740-274-6
17	86	4.5	532	4	US-09-252-991A-25188
18	85.5	4.5	270	2	US-08-773-368-1
19	85.5	4.5	270	3	US-09-199-887-1
20	85.5	4.5	1056	2	US-08-627-873-7
21	85	4.4	288	4	US-09-270-767-43786
22	85	4.4	332	4	US-09-252-991A-21222
23	85	4.4	755	5	PCT-US93-07923-3
24	85	4.4	759	5	PCT-US93-07923-2
25	85	4.4	766	1	US-08-230-491A-3
26	85	4.4	766	1	US-08-619-280A-3
27	85	4.4	766	2	US-08-940-391-3

ALIGNMENTS

RESULT 1

US-09-949-016-10038
; Sequence 10038, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10038
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10038

Query Match 18.8%; Score 360.5; DB 4; Length 348;
Best Local Similarity 33.9%; Pred. No. 3.9e-32;
Matches 100; Conservative 44; Mismatches 100; Indels 51; Gaps 12;
QY 17 FEGYKRLITSEAPVFDPHGSLRLSRSID-----SVLDLA----- 57
DB 21 FEGTKLEWFSRQPDANQSGDLRTIPRSEWDLKDVQCSIIISVTKDKQEAIVLS 80
QY 58 -----RKIVKTCGTTKLITIPRIELAEELS--NPLAAVKYSRGTFIFPQAOPAP 107
DB 81 ESSMFVKRFRILTKCTGILLKALVPLKLRDYSGFDSIQGFYSRKNKMPKSHQGY 140
QY 108 HRSFSBEAVLNRYFGKLSGGNAYVIGDAARPGQKWHIYYATEYPE-----QPMVNLEM 162
DB 141 HRNFQIEIFLNAIF---PNGAAYCMG--RWNSDCMYL-YTLDFPESRVISQDQTL 193
QY 163 CMTGLDTKASVFFKTNADGNTTCAKEMTKLSGISIIIEIMEICDFDFPCGCGSMAIHG 222
DB 194 LMSLDPVMDQFYM--KDGVT--AKDVTRESGIRDLIFGSVIDATMFPNCPGSMGMS 249
QY 223 -SAFSTIHTVTPDEGFSYASVEVMGLDATALSYGLVKRVLGCGFSPSEFSVAVTIF 276
DB 250 DGTWTIHITPEPEFSYVSFET---NLSQTSYDLDLRKVVVEPKGKF--VTTLF 299

RESULT 2

US-09-917-254-54
; Sequence 54, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224 (JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 54
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-917-254-54

Query Match 18.6%; Score 356.5; DB 4; Length 334;
Best Local Similarity 33.6%; Pred. No. 1e-31;
Matches 99; Conservative 44; Mismatches 101; Indels 51; Gaps 12;
QY 17 FEGYERKLEITFSEAPVFVDPHGSGLRALRSQID-----SVLDLA----- 57
DB 7 FEGTEKLEVFQRQPDANQSGDLRTIPRSEWDILLKDVQCSIIISVTKTQOEAYVLS 66
QY 58 -----RKIVTKCTGTTKLLLTIPRILELAELS--MPLAAVKYSRGTFIFPGAPAP 107
DB 67 ESSMFVSKRRFIKTKGTTLLKALVPLKLDYSGFDSIQSFYRKRKMFPSHQYP 126
QY 108 HRSFSEVAVLNRYFGGLSGGNAYVIGDAARPGQKWHIYATEYPE-----QPMVNLEM 162
DB 127 HRNFQEEIEFLNAIF---PNGAGYCMG--RMNSDCWYL-YTLDFPESRVISQPDQTL 179
QY 163 CMTGLDTKASVFYKTNADGNTTCAKEMTKLSGISILPMEICDFDFPFCGYSMAIHG 222
DB 180 LMSGLDPAVMDQPYM--KQGV--AKDVTRESGIRDLPGSVIDATMFNFCGYSMNGMS 235
QY 223 -SAFSTHVTPEGDFGSYASVEVMGLDATALSYGDLVKRVLGCGFSPSEFVATIF 276
DB 236 DGYTWIHIHTEPEFSYVSEF--NLSQTSYDLDLRKVEVPKPKGF--VTILF 285

RESULT 3

US-09-248-796A-18169
; Sequence 18169, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18169
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18169

Query Match 17.3%; Score 331; DB 4; Length 424;
Best Local Similarity 29.9%; Pred. No. 1.3e-28;
Matches 100; Conservative 49; Mismatches 98; Indels 88; Gaps 13;
QY 13 SAIGFEGYERKLEITFSE-----APVFVDP-----HGSGLRALSQID---- 51

Db 61 SHAFEGPEKLEIWFYSEKELSPINLRDIKPDFTWIEILNLHVCEVLKSVSSNLCAFL 120
QY 52 ----SVLDLARKIVIKTCGTTKLLLTIPRILE-LABEL-----SMPLAAVKYSRG 96
Db 121 SSSLFVFPFKIILKTCGTTTTLACLDLLEFETVNKELLQNEGLKATFQSKNIYQIFYSRR 180
QY 97 TFIFFGAQAPHRSPSEYAVLNRYFGGLKSGGNAYVIGDAARPGQKWHIY----- 148
Db 181 SFMFPDRQIHVHGNWQEEVKLLNQYF-----NNGKSYIVGN-----NTNWHLYVGNKGTKN 232
QY 149 ----ATEYPEQPMVN---LEMCMTGTLDTTKKASVFFKTNADGNTT-----CAKEMT 191
Db 233 PVASTTTTTTTPVNDCTLEIIMTQLSLEASQOFTYTRKEGDTAIDSNHDLGHLQOEIL 292
QY 192 KLSGISIEL-----PEMEICD-FDFPFCGYSMAIHGSAFSTHVTPEGDF 236
Db 293 KQTGLNELFKKQPTMPGLSSSPIKEIHDFGFAFTPCGFSNSINESNYTYIHTVPEPGW 352
QY 237 SYASVEVMGLDATALSYGDLVKRVLGCGFSPSEFV 271
Db 353 SYASFETNMIG----DYKAIVDKCINNVFQPGPMV 383

RESULT 4

US-09-902-540-11867
; Sequence 11867, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11867
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11867

Query Match 5.1%; Score 97.5; DB 4; Length 350;
Best Local Similarity 20.8%; Pred. No. 0.042;
Matches 55; Conservative 30; Mismatches 111; Indels 69; Gaps 9;
QY 144 WHIYATEYPEQPMVNLEMCMTGTLDTTKKASVFFKTNADGNTTCAKEMTKLSGISILPEM 203
Db 37 WHV--SNVFSQPDILAAQLTWSGLSRAFCNCGAEEALLKTRKVMKDRGTPERF 94
QY 204 EICDPDFPFCGYSMAIHGSAFSTHVTPEGDFGSYASVEVMGLDATALSYGDLVKRVLGC 263
Db 95 EVISFD-----SSFHGTLTATVATGQAKYQ-KGFPELPAGFTHVPYCDL-EAVRKA 144
QY 264 FGFSEFSVAVTIFFGGRGQA-----GTWKGELGAE 292
Db 145 VGPATAAILVEPIQEGGVRMAPLFLVGLRALCDEHGLLLLVDEVTGMRGKPGF- 203
QY 293 AYDCNNVQEQLP-----GGGILLYQSFCAAEDAVASSPKSVLCDFGDNAPFAK 343
Db 204 -----MHEGIVDPDGISVAKALGNGLPIGAMLCKEELGASLTPTGHTSGFNGNFAAAA- 256
QY 344 DCKLANLVCLXEEXDAIEEKDGVLD 368
Db 257 ----ANAV-----RILRRPGFLDE 272
RESULT 5
US-09-010-877-2


```
; Sequence 2, Application US/09010877B
; Patent No. 6444445
; GENERAL INFORMATION:
; APPLICANT: Walter Reed Army Institute of Research
; APPLICANT: Nikolich, Mikeljon
; APPLICANT: Hoover, David L.
; APPLICANT: Warren, Richard L.
; APPLICANT: Lindler, Luther E.
; APPLICANT: Hadfield, Ted L.
; APPLICANT: Boyle, Stephen M.
; APPLICANT: McQuiston, John R.
; APPLICANT: Schurig, Gerhard G.
; APPLICANT: Nammalwar Sriranganathan
; TITLE OF INVENTION: Live Vaccines Against Brucellosis
; FILE REFERENCE: Army-124
; CURRENT APPLICATION NUMBER: US/09/010,877B
; EARLIER APPLICATION NUMBER: NO. 6444445e
; EARLIER FILING DATE: NO. 6444445e
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PC-IBM compatible
; SEQ ID NO 2
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Brucella abortus
US-09-010-877-2

Query Match      5.0%; Score 96.5; DB 4; Length 410;
Best Local Similarity 24.0%; Pred. No. 0.072;
Matches 47; Conservative 28; Mismatches 82; Indels 39; Gaps 9;

QY 98 FIFGQAPAPRHSFSEVAVLNRYFGLKSGGNAYVIGDAA---RPGQKWHIYYATEYPE 154
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 217 FLMP-TNPNAKHAKAFQALDIYYGKLGKIKTKIVGVSSVRMDPSHRQAKYEN---K 272
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 155 QPMVNLEMCMTGLDTTKASVYFF-----KTNADGNNTCAKEMTKL 193
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 273 AVYKSVREIVAGLDNLKSNVEFAGEVADKEYAEILLASACFFMPTLADNGTFAAVEAAYM 332

QY 194 S--GISEIIPMEICDFDFE-PCGYSMNAIH---GSAFTIHVTPEDGFSYASYEVMGL 246
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 333 GCPTLNDYPMQRYISNRFPIPMQY-FNARSVKEMASALKQMBETPIDVGLLPSRETLSL 391

QY 247 ---DATALSVDLVR 259
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 392 HSWEARHASEYWDIVR 407

RESULT 6
US-09-710-279-874
; Sequence 874, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 874
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-09-710-279-874

Query Match      4.9%; Score 94.5; DB 4; Length 331;
Best Local Similarity 22.7%; Pred. No. 0.085;
Matches 45; Conservative 32; Mismatches 68; Indels 53; Gaps 9;

QY 147 YYATEYPEQPMVNLEMCMTGLDTTKASVFFKTNADGNNTCA-----KEMT 191
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 FIQTNPQNPFFYNKAMCVCGTGGDSNSP-----NISTTVAFVVASAGVPVIKHGNSIT 113

QY 192 KLSGISEIIPMEICDFDFEPCGYSMNAIHGSAFSTIHVTPEDGF-----SYAS 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 114 SHSGSTDVLHEMNIKTNKMEVEQQLN-LKGLAF-----ISATDSYPMKKLQSIKSIAT 168

QY 241 YEVMGLDATALSYGDLVKKVLCFGFSEF-SVAVTIFGGRGQAGTWGKELGAE----AYD 295
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 169 PTIFNLIGPLINPFKLTYYQVMGYVEASOLENIAQTL-----KDLGRKRAILING 217

QY 296 CNNMVEQELPGGGILIYQ 313
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 218 ANGMDAATLSGENI-IYE 234

RESULT 7
US-09-710-279-2244
; Sequence 2244, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2244
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-09-710-279-2244

Query Match      4.9%; Score 94.5; DB 4; Length 331;
Best Local Similarity 22.7%; Pred. No. 0.085;
Matches 45; Conservative 32; Mismatches 68; Indels 53; Gaps 9;

QY 147 YYATEYPEQPMVNLEMCMTGLDTTKASVFFKTNADGNNTCA-----KEMT 191
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 FIQTNPQNPFFYNKAMCVCGTGGDSNSP-----NISTTVAFVVASAGVPVIKHGNSIT 113

QY 192 KLSGISEIIPMEICDFDFEPCGYSMNAIHGSAFSTIHVTPEDGF-----SYAS 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 114 SHSGSTDVLHEMNIKTNKMEVEQQLN-LKGLAF-----ISATDSYPMKKLQSIKSIAT 168

QY 241 YEVMGLDATALSYGDLVKKVLCFGFSEF-SVAVTIFGGRGQAGTWGKELGAE----AYD 295
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 169 PTIFNLIGPLINPFKLTYYQVMGYVEASOLENIAQTL-----KDLGRKRAILING 217

QY 296 CNNMVEQELPGGGILIYQ 313
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 218 ANGMDAATLSGENI-IYE 234

RESULT 8
US-09-134-001C-5198
; Sequence 5198, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
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```
; Sequence 2, Application US/09010877B
; Patent No. 6444445
; GENERAL INFORMATION:
; APPLICANT: Walter Reed Army Institute of Research
; APPLICANT: Nikolich, Mikeljon
; APPLICANT: Hoover, David L.
; APPLICANT: Warren, Richard L.
; APPLICANT: Lindler, Luther E.
; APPLICANT: Hadfield, Ted L.
; APPLICANT: Boyle, Stephen M.
; APPLICANT: McQuiston, John R.
; APPLICANT: Schurig, Gerhard G.
; APPLICANT: Nammalwar Sriranganathan
; TITLE OF INVENTION: Live Vaccines Against Brucellosis
; FILE REFERENCE: Army-124
; CURRENT APPLICATION NUMBER: US/09/010,877B
; EARLIER APPLICATION NUMBER: NO. 6444445e
; EARLIER FILING DATE: NO. 6444445e
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PC-IBM compatible
; SEQ ID NO 2
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Brucella abortus
US-09-010-877-2

Query Match      5.0%; Score 96.5; DB 4; Length 410;
Best Local Similarity 24.0%; Pred. No. 0.072;
Matches 47; Conservative 28; Mismatches 82; Indels 39; Gaps 9;

QY 98 FIFGQAPAPRHSFSEVAVLNRYFGLKSGGNAYVIGDAA---RPGQKWHIYYATEYPE 154
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 217 FLMP-TNPNAKHAKAFQALDIYYGKLGKIKTKIVGVSSVRMDPSHRQAKYEN---K 272
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 155 QPMVNLEMCMTGLDTTKASVYFF-----KTNADGNNTCAKEMTKL 193
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 273 AVYKSVREIVAGLDNLKSNVEFAGEVADKEYAEILLASACFFMPTLADNGTFAAVEAAYM 332

QY 194 S--GISEIIPMEICDFDFE-PCGYSMNAIH---GSAFTIHVTPEDGFSYASYEVMGL 246
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 333 GCPTLNDYPMQRYISNRFPIPMQY-FNARSVKEMASALKQMBETPIDVGLLPSRETLSL 391

QY 247 ---DATALSVDLVR 259
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 392 HSWEARHASEYWDIVR 407

RESULT 6
US-09-710-279-874
; Sequence 874, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 874
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-09-710-279-874

Query Match      4.9%; Score 94.5; DB 4; Length 331;
Best Local Similarity 22.7%; Pred. No. 0.085;
Matches 45; Conservative 32; Mismatches 68; Indels 53; Gaps 9;

QY 147 YYATEYPEQPMVNLEMCMTGLDTTKASVFFKTNADGNNTCA-----KEMT 191
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 FIQTNPQNPFFYNKAMCVCGTGGDSNSP-----NISTTVAFVVASAGVPVIKHGNSIT 113

QY 192 KLSGISEIIPMEICDFDFEPCGYSMNAIHGSAFSTIHVTPEDGF-----SYAS 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 114 SHSGSTDVLHEMNIKTNKMEVEQQLN-LKGLAF-----ISATDSYPMKKLQSIKSIAT 168

QY 241 YEVMGLDATALSYGDLVKKVLCFGFSEF-SVAVTIFGGRGQAGTWGKELGAE----AYD 295
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 169 PTIFNLIGPLINPFKLTYYQVMGYVEASOLENIAQTL-----KDLGRKRAILING 217

QY 296 CNNMVEQELPGGGILIYQ 313
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 218 ANGMDAATLSGENI-IYE 234

RESULT 7
US-09-710-279-2244
; Sequence 2244, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2244
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-09-710-279-2244

Query Match      4.9%; Score 94.5; DB 4; Length 331;
Best Local Similarity 22.7%; Pred. No. 0.085;
Matches 45; Conservative 32; Mismatches 68; Indels 53; Gaps 9;

QY 147 YYATEYPEQPMVNLEMCMTGLDTTKASVFFKTNADGNNTCA-----KEMT 191
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 FIQTNPQNPFFYNKAMCVCGTGGDSNSP-----NISTTVAFVVASAGVPVIKHGNSIT 113

QY 192 KLSGISEIIPMEICDFDFEPCGYSMNAIHGSAFSTIHVTPEDGF-----SYAS 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 114 SHSGSTDVLHEMNIKTNKMEVEQQLN-LKGLAF-----ISATDSYPMKKLQSIKSIAT 168

QY 241 YEVMGLDATALSYGDLVKKVLCFGFSEF-SVAVTIFGGRGQAGTWGKELGAE----AYD 295
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 169 PTIFNLIGPLINPFKLTYYQVMGYVEASOLENIAQTL-----KDLGRKRAILING 217

QY 296 CNNMVEQELPGGGILIYQ 313
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 218 ANGMDAATLSGENI-IYE 234

RESULT 8
US-09-134-001C-5198
; Sequence 5198, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
```

1

Matches 95; Conservative 51; Mismatches 124; Indels 174; Gaps 24;

QY 35 VDPHSGS-----LRLASRS-----QIDSVLDLA--RKIVIKTCGTTKLLI--- 72

Db 861 VETHGTGTRLDPIEARLSDAYGGDEHPLRGSVKSNIGHTQAAGVAGLIKLVLMQ 920

QY 73 --TIPRIELAEBSLPLAAVKYSGTFIF---PGAQAPHRFSBEVAVLNRYFGGLKS 127

Db 921 AGVLPRTLHADE---PSPEIDSSGAISLLOEPAAMPAGERPRRAGVS---SFG--IS 970

QY 128 GGNAYVI-----GDAARPGQ-----KWHIYYAT-----EYEPQPMVN 159

Db 971 GTNAHAIIIEAPTGDTRDRMGVPVPMVLSASTGEALRAARLAGHLRHPDQ---D 1027

QY 160 LEMCTGLDTPKASVFFKTN---ADGNTTCAKEMTKLSGISEIIPEMEICDFDFEPCGYS 216

Db 1028 LDDVAYSLATGRAALAYRSFVPADASTAL-----RILDEL-----AAGS 1068

QY 217 MNAIHGSFAS---TIHVTPEGFSYASYEVNGLD-----ATAL----- 251

Db 1069 GDAVTGTARAPQWVFFPCGQWAGMAVDLDDGPFVASFASVLRCEADALEPYLDPEIVP 1128

QY 252 -----SYGDLKRVLCGFPSEFSVAVTI-----FG-----GRGQ 281

Db 1129 FLRAEAQRTPDHTLSTRDVRVQPVVL-----FAMVSLAARWRAYGVEPAAVIGHSQ 1181

QY 282 -----ACTWKGKELGAEAYDCNNMVEQBLPGGGLIYQSCAAEDAVA----- 323

Db 1182 GETAACVAGALSDDAARAVALSRSVIATMPNGAM--ASIAASVDEVAARIDGRVEIA 1239

QY 324 --SSPKSVLRFCFGDGENAAPKDC 345

Db 1240 AVNGPRAVVVSGDRDDLRLVASC 1263

RESULT 12

US-08-008-688A-2

Sequence 2, Application US/08008688A

Patent No. 5462862

GENERAL INFORMATION:

APPLICANT: Martinus A. M. Groenen

APPLICANT: Annemarie E. Veenstra

APPLICANT: Pieter Van Solingen

APPLICANT: Bertus P. Koekman

APPLICANT: Lucia H. M. Van Der Voort

APPLICANT: Juan F. Martin

APPLICANT: Santiago Gutierrez

APPLICANT: Bruno Diez

APPLICANT: Emilio Alvarez

APPLICANT: Jose L. Barredo

APPLICANT: Christina Esmahan

TITLE OF INVENTION: A METHOD FOR ENHANCING PRODUCTION OF

TITLE OF INVENTION: SECONDARY METABOLITES USING

TITLE OF INVENTION: CLUSTERED BIOSYNTHETIC GENES

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson

STREET: 2200 Sand Hill Road, Suite 100

CITY: Menlo Park

STATE: California

COUNTRY: U.S.A.

ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 502 or 55SX

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/008,688A

FILING DATE: 19930125

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/392,119

FILING DATE: August 10, 1989

APPLICATION NUMBER: EPO 88201714.8

FILING DATE: August 11, 1988

APPLICATION NUMBER: EPO 89201044.8

FILING DATE: April 21, 1989

ATTORNEY/AGENT INFORMATION:

NAME: Barbara Rae-Venter

REGISTRATION NUMBER: 32,750

REFERENCE/DOCKET NUMBER: 05939/024002

TELEPHONE: (415) 854-5277

TELEFAX: (415) 854-0875

TELEX: ---

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 355

TYPE: amino acid

STRANDEDNESS: N/A

TOPOLOGY: N/A

US-08-008-688A-2

Query Match 4.5%; Score 86.5; DB 1; Length 355;

Best Local Similarity 22.7%; Pred. No. 0.78;

Matches 82; Conservative 45; Mismatches 117; Indels 117; Gaps 21;

QY 17 FE-GYEKRLEITFSEAPVFDPHGSLRALRSQIDSVLDLARKIVIKTCGTTKLLI-I 74

Db 9 FEIGYE-----HGSAAKAVIARSIDPAVDLIRGKTKTKTDEELKQVLSQL 52

QY 75 PRILE-----LAEBSLPLAAVKYSGTFIFPGAQAPHRFSBEVAVLN---RYFGGLK 126

Db 53 GRVIERWPKYEEI-----RG--IAKGAE-----RDVS-EIVMLNTRTEFAYGLK 95

QY 127 SGN-----AYV-IGDAARPGQKWHIYYATEYEPQPMVNLEMCTGLDTPKASVFFKTNAD 181

Db 96 AARDGCTTAYCOLPNGALQONQYDFFSAT---KENLIRLTIRQAGLPTIK---FITEA- 147

QY 182 GNTTCAKEMTKLSGISEIIPEMEICDFEPCGYSMNAIHGSASFSTIHVTPEDGFSYASY 241

Db 148 -----GI-----IGKVGNSAGAVN-----YNAL 167

QY 242 EVMGLDATALSYGDLVKRVLCGFPSEFSVAVTIFFGGRG-----QAGTWKGKELGAEAYDC 296

Db 168 HLQGLRPTGVPVSHIALRIALSTSPSQAYDRIVEQGGMAASAFIMVGNHGAFCLE-FSP 226

QY 297 NNWVEQELPGGGLIYQSCAA-----EDAVASSPKS-----VLRCFDGENAAPFA 342

Db 227 TSIRKQVLDANGRMVHTNHCLLQHKNEKELDPLDPSWNRHORMEFLLDGFDGTTKQA-FA 285

QY 343 K 343

Db 286 Q 286

RESULT 13

US-09-604-957-4

Sequence 4, Application US/09604957

Patent No. 6486314

GENERAL INFORMATION:

APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA

APPLICANT: DIJKHUIZEN, LUBBERT

APPLICANT: RAHAOUI, HAKIM

APPLICANT: LEER, ROBERT-JAN

TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASE AND NOVEL GLUCAN

FILE REFERENCE: BO 43388

CURRENT APPLICATION NUMBER: US/09/604,957

CURRENT FILING DATE: 2000-06-28

PRIOR APPLICATION NUMBER: 00201871.1

PRIOR FILING DATE: 2000-05-25

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patent in Ver. 2.1

SEQ ID NO 4

```
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-09-604-957-4

Query Match
 4.5%; Score 86.5; DB 4; Length 545;
Best Local Similarity 22.5%; Pred. No. 1.6;
Matches 73; Conservative 50; Mismatches 137; Indels 65; Gaps 17;

QY 33 VFVDPHGSLRALSRSQIDSVLDLARKIVIKTCGTTKLLTIPRIILELAELSMPAAVK 92
Db 158 IFIRAHDSVQTVIAKIKA-----QINPKTDGLTFTLDELQAQFIYNE-DMRQAKK 210

QY 93 YSRGTTFPGAQAPAPHR-SFSEEVAVLNRYFGGLKSGGNAYVIG-----DAARPQKWHI 146
Db 211 YTQSN-----PTAYALMSLNKDSITRLYGYDMYSDGQYMATKSPYYDAITLLKARI 264

QY 147 YYAT-----EYPEQPMWNLKMTGLDTKKASVFFKTNADGNTTCAKEMTKLSGISEI 199
Db 265 KYAAGQDMKITTVGDKSHMDYTGVL-----SVRYGTGANATDQGSATKTQGNVAVI 321

QY 200 I---PEMEICDFPEPCGYSMNAIH-GSAFSTIHVTPEDGF-SYASYEVNGLDATALSY- 253
Db 322 TSNPSSLKLNQND--KVIVNMGAAHKNQOEYRPLLLTTKDLGTSYTS-----DAAAKSLY 373

QY 254 -----GDLV---KRVLGCGFGP---SEFSVAVTIFFGRGQ-----AGTWGKELGAEAYDCN 297
Db 374 RKTNDKGLVDFDASDIQGYLNPQVSGYLAVWVPVGASDNDQVRVAASNKANATGQVYESS 433

QY 298 NMVEQELPGGGILLIYOSFCAAEADAV 322
Db 434 SALDSQ-----LIYEGFSNFQDFV 452

RESULT 14
US-09-008-172-2
; Sequence 2, Application US/09008172
; Patent No. 6127602
; GENERAL INFORMATION:
; APPLICANT: Nichols, Scott E.
; TITLE OF INVENTION: Substitutes for Modified Starch and
; FILE REFERENCE: 0358D
; CURRENT APPLICATION NUMBER: US/09/008,172
; EARLIER FILING DATE: 1998-01-16
; EARLIER APPLICATION NUMBER: 08/482,711
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1430
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-09-008-172-2

Query Match
 4.5%; Score 86.5; DB 3; Length 1430;
Best Local Similarity 22.5%; Pred. No. 8.2;
Matches 73; Conservative 50; Mismatches 137; Indels 65; Gaps 17;

QY 33 VFVDPHGSLRALSRSQIDSVLDLARKIVIKTCGTTKLLTIPRIILELAELSMPAAVK 92
Db 578 IFIRAHDSVQTVIAKIKA-----QINPKTDGLTFTLDELQAQFIYNE-DMRQAKK 630

QY 93 YSRGTTFPGAQAPAPHR-SFSEEVAVLNRYFGGLKSGGNAYVIG-----DAARPQKWHI 146
Db 631 YTQSN-----PTAYALMSLNKDSITRLYGYDMYSDGQYMATKSPYYDAITLLKARI 684

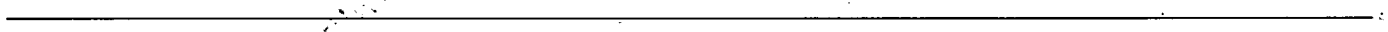
QY 147 YYAT-----EYPEQPMWNLKMTGLDTKKASVFFKTNADGNTTCAKEMTKLSGISEI 199
Db 685 KYAAGQDMKITTVGDKSHMDYTGVL-----SVRYGTGANATDQGSATKTQGNVAVI 741

QY 200 I---PEMEICDFPEPCGYSMNAIH-GSAFSTIHVTPEDGF-SYASYEVNGLDATALSY- 253
Db 742 TSNPSSLKLNQND--KVIVNMGAAHKNQOEYRPLLLTTKDLGTSYTS-----DAAAKSLY 793

QY 254 -----GDLV---KRVLGCGFGP---SEFSVAVTIFFGRGQ-----AGTWGKELGAEAYDCN 297
Db 794 RKTNDKGLVDFDASDIQGYLNPQVSGYLAVWVPVGASDNDQVRVAASNKANATGQVYESS 853

QY 298 NMVEQELPGGGILLIYOSFCAAEADAV 322
Db 854 SALDSQ-----LIYEGFSNFQDFV 872

Search completed: May 11, 2005, 22:53:52
Job time : 25.3436 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 11, 2005, 22:36:02 ; Search time 93.8969 Seconds
(without alignments)
1515.788 Million cell updates/sec

Title: US-10-732-923-407

Perfect score: 1914

Sequence: 1 MAVLSAAGAPPASAIAGFEY.....NLVCLFEXDAIEEKDGLVDS 368

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1990s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1853	96.8	366	8	Adm48039 Polypepti
2	1726	90.2	400	8	Adm48040 Polypepti
3	862.5	45.1	237	7	Abm73860 DNA clone
4	804.5	42.0	360	2	Aar75006 Tomato S-
5	802	41.9	363	5	Aau79674 Cucurbita
6	802	41.9	363	8	Abg75228 Plant wit
7	802	41.9	363	8	Adp90956 Fig leaf g
8	802	41.9	363	8	Adr38366 Fig leaf
9	771.5	40.3	366	3	Rag28816 Arabidops
10	737	38.5	309	7	Abm73938 DNA clone
11	455	23.8	155	7	Abm74096 DNA clone
12	425.5	22.2	215	3	Rag28817 Arabidops
13	393.5	20.6	184	3	Rag28818 Arabidops
14	377.5	19.7	368	8	Adn22644 Bacterial
15	377.5	19.7	368	8	Adn22643 Bacterial
16	360.5	18.8	348	3	Aab56589 Human pro
17	359	18.8	348	4	Abg05997 Novel hum
18	356.5	18.6	334	5	Aau84313 Protein A
19	356.5	18.6	334	7	Adm60574 Human Pro
20	356.5	18.6	334	7	Add48325 Human Pro
21	356.5	18.6	334	7	Adm60570 Human Pro
22	356.5	18.6	334	7	Add48321 Human Pro
23	356.5	18.6	334	8	Adn03708 Antipori
24	356.5	18.6	334	8	Adq88208 Human 912
25	356.5	18.6	347	4	Abb61186 Drosophil

26	355.5	18.6	333	7	Adm60568 Rat Prote
27	355.5	18.6	333	7	Add48323 Rat Prote
28	355.5	18.6	333	7	Adm60572 Rat Prote
29	355.5	18.6	333	7	Add48319 Rat Prote
30	346	18.1	369	8	Adn19900 Bacterial
31	334	17.5	478	8	Adg92091 Fungal S-
32	324.5	17.0	493	7	Adm07131 Aspergill
33	324.5	17.0	493	7	Adm07012 Aspergill
34	294	15.4	396	8	Adm48038 Polypepti
35	294	15.4	396	8	Adm48038 Polypepti
36	290	15.2	503	8	Adn20733 Bacterial
37	156	8.2	184	8	Adm6385 Novel hum
38	124.5	6.5	196	4	Abg05996 Novel hum
39	116	6.1	773	4	Abg30328 Novel hum
40	104	5.4	1297	4	Abg05671 Novel hum
41	103.5	5.4	4640	7	Adj70297 Human hea
42	101.5	5.3	339	6	Abm67983 Phototrab
43	97.5	5.1	394	8	Adm30448 Bacterial
44	96.5	5.0	410	2	Aay28354 Ribu, a m
45	96.5	5.0	410	8	Adp71263 Brucella

ALIGNMENTS

RESULT 1
ADM48039
ID ADM48039 standard; protein; 366 AA.

AC ADM48039;

DT 03-JUN-2004 (first entry)

DE Polypeptide sequence #89 useful in producing transgenic plants.

Plant; maize; rice; sorghum; thale cress; soybean; wheat; transgenic;
osmotic stress; sugar transport; cell cycle pathway; plant height;
carbohydrate transport; crop productivity; plant growth;
stress resistance; disease resistance; insect resistance; heat tolerance;
nitrogen assimilation; water stress tolerance;
photosynthetic carbon fixation; virus resistance; gene therapy.
Zea mays.

US2003233670-A1.

18-DEC-2003.

04-DEC-2002; 2002US-00310154.

04-DEC-2001; 2001US-0337358P.

(EDGE/) EDGERTON M D.

(CHOM/) CHOMET P S.

(LACC/) LACCETTI L B.

Edgerton MD, Chomet PS, Laccetti LB;

WPI; 2004-061374/06.

N-PSDB; ADM47671.

New polynucleotide, useful for manipulating plant protein quality,
improving plant growth, yield and crop productivity or grain composition
or producing plants with improved properties.

Claim 8; SEQ ID NO 457; 144pp; English.

The present invention relates to polynucleotide sequences, and the
proteins they encode. The sequences are isolated from a variety of
organisms such as plants (e.g. maize, rice, sorghum, thale cress,
soybean, and wheat), cyanobacteria, bacteria, yeast and other fungi. The
polynucleotide and polypeptide sequences of the invention are useful in
the production of transgenic plants that have improved properties. Also

CC disclosed are methods of producing fertile transgenic plants, preferably
 CC maize, with desired phenotypes. The polynucleotide and polypeptide
 CC sequences are useful for improving plants by providing protection against
 CC osmotic stress, improving altering sugar transport and/or metabolism,
 CC modifying the cell cycle pathway, reducing plant height, modifying
 CC carbohydrate transport, improving crop productivity, improving plant
 CC growth and stress resistance, improving disease resistance, improving
 CC insect resistance, improving cold or heat tolerance, improving nitrogen
 CC assimilation, improving stalk strength, improving water stress tolerance,
 CC improving photosynthetic carbon fixation, improving biotic and abiotic
 CC stress resistance, improving resistance to oxidative stress, providing
 CC increased vigour, reducing senescence, and conferring virus resistance.
 CC The present sequence represents a polypeptide sequence of the invention.
 CC Note: The sequence data for this patent is not provided in the printed
 CC specification but is obtained in electronic format from the USPTO website
 CC at seqdata.uspto.gov.

XX
 SQ Sequence 366 AA;

Query Match 96.8%; Score 1853; DB 8; Length 366;
 Best Local Similarity 100.0%; Pred. No. 2.2e-192;
 Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAVLSAAGAPPASAIAGFEGYEKLEITFSEAPVDPHGSLRALSRQSDSVLDLARKI 60
 DB 1 MAVLSAAGAPPASAIAGFEGYEKLEITFSEAPVDPHGSLRALSRQSDSVLDLARKI 60
 QY 61 VIKTCGTTKLLLTIPRIELAEBSLPLAAVKYSRGTFIPFGAQPAPHRFSFEVAVLNR 120
 DB 61 VIKTCGTTKLLLTIPRIELAEBSLPLAAVKYSRGTFIPFGAQPAPHRFSFEVAVLNR 120
 QY 121 YFGLKSGGNAYVIGDAARPGQKWHIYYATEYEPQWNLNEMCMTGLDTHKASVFFKTN 180
 DB 121 YFGLKSGGNAYVIGDAARPGQKWHIYYATEYEPQWNLNEMCMTGLDTHKASVFFKTN 180
 QY 181 DGNNTCAKEMTKLSGISEIPEIMEICDFPEPCGYSNNAIHGSAFSTIHVTPEDGFSYAS 240
 DB 181 DGNNTCAKEMTKLSGISEIPEIMEICDFPEPCGYSNNAIHGSAFSTIHVTPEDGFSYAS 240
 QY 241 YEVMGLDATALSYGDLVKRVLCGFGSFSFSAVTFEGGRQAGTWGKELGAEAYDCNNMV 300
 DB 241 YEVMGLDATALSYGDLVKRVLCGFGSFSFSAVTFEGGRQAGTWGKELGAEAYDCNNMV 300
 QY 301 EQELPGGGLIYQSFCAAEADAVASSPKSVLRCDFGGENAAPPKOCKLANLVCLLE 355
 DB 301 EQELPGGGLIYQSFCAAEADAVASSPKSVLRCDFGGENAAPPKOCKLANLVCLLE 355

RESULT 2
 ADM48040

ID ADM48040 standard; protein; 400 AA.

XX
 AC ADM48040;

XX
 DT 03-JUN-2004 (first entry)

XX
 DE Polypeptide sequence #90 useful in producing transgenic plants.

XX plant; maize; rice; sorghum; thale cress; soybean; wheat; transgenic;
 KW osmotic stress; sugar transport; cell cycle pathway; plant height;
 KW carbohydrate transport; crop productivity; plant growth;
 KW stress resistance; disease resistance; insect resistance; heat tolerance;
 KW nitrogen assimilation; water stress tolerance;
 KW photosynthetic carbon fixation; virus resistance; gene therapy.

XX
 OS Zea mays.

XX
 PN US2003233670-A1.

XX
 PD 18-DEC-2003.

XX
 PF 04-DEC-2002; 2002US-00310154.

XX

PR 04-DEC-2001; 2001US-0337358P.

XX (EDGE/) EDGERTON M D.
 PA (CHOM/) CHOMET P S.
 PA (LACC/) LACCETTI L B.

PI Edgerton MD, Chomet PS, Laccetti LB;

XX WPI; 2004-061374/06.
 DR N-PSDB; ADM47672.

XX New polynucleotide, useful for manipulating plant protein quality,
 PT improving plant growth, yield and crop productivity or grain composition
 PT or producing plants with improved properties.

XX Claim 8; SEQ ID NO 458; 144pp; English.

XX The present invention relates to polynucleotide sequences, and the
 CC proteins they encode. The sequences are isolated from a variety of
 CC organisms such as plants (e.g. maize, rice, sorghum, thale cress,
 CC soybean, and wheat), cyanobacteria, bacteria, and other fungi. The
 CC polynucleotide and polypeptide sequences of the invention are useful in
 CC the production of transgenic plants that have improved properties. Also
 CC disclosed are methods of producing fertile transgenic plants, preferably
 CC maize, with desired phenotypes. The polynucleotide and polypeptide
 CC sequences are useful for improving plants by providing protection against
 CC osmotic stress, improving altering sugar transport and/or metabolism,
 CC modifying the cell cycle pathway, reducing plant height, modifying
 CC carbohydrate transport, improving crop productivity, improving plant
 CC growth and stress resistance, improving disease resistance, improving
 CC insect resistance, improving cold or heat tolerance, improving nitrogen
 CC assimilation, improving stalk strength, improving water stress tolerance,
 CC improving photosynthetic carbon fixation, improving biotic and abiotic
 CC stress resistance, improving resistance to oxidative stress, providing
 CC increased vigour, reducing senescence, and conferring virus resistance.
 CC The present sequence represents a polypeptide sequence of the invention.
 CC Note: The sequence data for this patent is not provided in the printed
 CC specification but is obtained in electronic format from the USPTO website
 CC at seqdata.uspto.gov.

XX Sequence 400 AA;

Query Match 90.2%; Score 1726; DB 8; Length 400;
 Best Local Similarity 84.5%; Pred. No. 1.7e-178;

Matches 338; Conservative 8; Mismatches 22; Indels 32; Gaps 3;

QY 1 MAVLSAAGAPPASAIAGFEGYEKLEITFSEAPVDPHGSLRALSRQSDSVLDLARKI 58

DB 1 MAVLSAAGAPPASAIAGFEGYEKLEITFSEAPVDPHGSLRALSRQSDSVLDLARKI 60

QY 59 -----KIVINTCGTTKLLLTIPRIELAEBSLPLAAVKY 93

DB 61 IVSELNKKDFDSYVLSSESLFIYPLKIVIKTCGTTKLLLTIPRIELAEBSLPLAAVKY 120

QY 94 SGTFTFPGQAOPAPHSFSEVAVLNRYFGLKSGGNAYVIGDAARPGQKWHIYYATEYP 153

DB 121 SGTFTFPGQAOPAPHSFSEVAVLNRYFGLKSGGNAYVIGDAARPGQKWHIYYATEYP 180

QY 154 EQPMVNLNEMCMTGLDTHKASVFFKTNADGNNTCAKEMTKLSGISEIPEIMEICDFDPEPC 213

DB 181 EQPMVNLNEMCMTGLDTHKASVFFKTNADGNNTCAKEMTKLSGISEIPEIMEICDFDPEPC 240

QY 214 GYSMNAIHGSAFSTIHVTPEDGFSYASYEVMGLDATALSYGDLVKRVLCGFGSFSFSAV 273

DB 241 GYSMNAIHGSAFSTIHVTPEDGFSYASYEVMGLDATALSYGDLVKRVLCGFGSFSFSAV 300

QY 274 TIFGGRGAGTWGKELGAEAYDCNNMVVEQLPGGGLIYQSFCAAEADAVASSPKSVLRCF 333

DB 301 TIFGGRGAGTWGKELGAEAYDCNNMVVEQLPGGGLIYQSFCAAEADAVASSPKSVLRCF 360

QY 334 DGENA-----APFAKOCKLANLVCL-EEXDAIEBKDGVLDE 368

DB 361 DGENVESAPPMKKDYKLANLLCWEEDAEADAMEEKAGVLDE 400


```
RESULT 3
ABM73860
ID ABM73860 standard; protein; 237 AA.
AC ABM73860;
XX
XX 17-OCT-2003 (first entry)
DT
DE DNA clone originating in barley containing SNP sequence #270.
XX
XX Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.
XX
XX Hordeum vulgare.
OS
XX W02003057877-A1.
PN
XX 17-JUL-2003.
PD
XX 16-DEC-2002; 2002WO-IB005403.
XX
XX 20-DEC-2001; 2001JP-00387059.
PR
XX 20-DEC-2001; 2001JP-00387131.
PR
XX 20-DEC-2001; 2001JP-00403299.
PR
XX 20-DEC-2001; 2001JP-00403300.
PR
XX 27-SEP-2002; 2002JP-00327515.
XX
XX (UYN1-) UNIV JAPAN OKAYAMA.
PA
XX
XX Sato K, Takeda K, Kohara Y;
PI
XX WPI; 2003-587127/55.
DR
XX
XX Single nucleotide polymorphism sites in barley varieties and DNA
PT sequences containing them for analysis and identification of barley
PT varieties and production of barley transformants with desired
PT characteristics.
XX
XX Disclosure; SEQ ID XX; 284pp; Japanese.
PS
XX
XX The present invention relates to oligonucleotide clones originating in
CC barley (Hordeum vulgare) which contain single nucleotide polymorphisms
CC (SNP). The oligonucleotides may be used for analysis of SNPs among barley
CC varieties, identification of particular varieties and genotype-phenotype
CC analysis, isolation of specific genes and creation of new varieties by
CC transformation of barley varieties with them and production of new barley
CC varieties with desired properties. The present sequence represents an
CC oligonucleotide clone sequence featured in the specification. The
CC specification data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published-pct-sequences
XX
XX Sequence 237 AA;
SQ
Query Match 45.1%; Score 862.5; DB 7; Length 237;
Best Local Similarity 77.5%; Pred. No. 8.6e-85;
Matches 172; Conservative 7; Mismatches 16; Indels 27; Gaps 1;
QY 9 APPASAI GEGYKRL EITFSEAPVFDPHGSLRALSRSQIDSVLDLAR----- 58
DB 2 AAPTSAI GEGYKRL EITFNEASIPADPHGRLRALSRAQIDSVLDLARCTIVSLSNK 61
QY 59 -----KIVIKTCGTTKLLITIPRIELAEELSMPAAVKYSGRTFIP 101
DB 62 DFDSYVLSSESLFYISQIKIVIKTCGTTKLLITIPRIELAEELSMPAAVKYSGRTFIP 121
QY 102 GAQAPHRSESEVAVLNRYFGGLKSGGNAYVIGDAARPGQKWHIYYATEYPEQPMVNL 161
DB 122 GAQAPHRSESEVAVLNRYFGHLKSGGNAYVIGDAARPGQKWHIYYATEYPEQPMVNL 181
QY 162 MCMTGLDTPKASVFFKTSADGNTTCAKEMTKLSGISNIIPEM 203
||||| ||||||| : : : : : ||||||| |||

Db 182 MCMTGLDTPKASVFFKTSADGHVSCAKEMTKLSGISNIIPEM 223

RESULT 4
AAR75006
ID AAR75006 standard; protein; 360 AA.
AC AAR75006;
XX
XX 25-MAR-2003 (revised)
DT
DT 01-NOV-1995 (first entry)
XX
XX Tomato S-adenosyl-methionine-decarboxylase.
DE
XX SAM-decarboxylase; transgenic plant; senescence; fruit ripening.
XX
XX Lycopersicon esculentum.
OS
XX W09514092-A1.
PN
XX 26-MAY-1995.
XX
XX 17-NOV-1994; 94WO-GB002532.
PR
XX 18-NOV-1993; 93GB-00023771.
XX
XX (ZENE ) ZENECA LTD.
PA
XX
XX Grierson D, Fray RG, Wallace AD;
PI
XX WPI; 1995-200382/26.
DR
XX N-PSDB; AAQ90508.
DR
XX
XX New S-adenosyl methionine-decarboxylase DNA - used to transform plants to
PT modify senescence and fruit-ripening characteristics.
XX
XX Disclosure; Page 25-26; 34pp; English.
PS
XX
XX DNA encoding SAM-decarboxylase is used to transform plants. Modifying SAM
CC decarboxylase (SAM) gene expression in transgenic plants modifies
CC senescence or fruit-ripening characteristics. Increased SAMD levels
CC reduce ethene production by the plant, and decreased SAMD levels increase
CC ethene production by the plant. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX Sequence 360 AA;
SQ
Query Match 42.0%; Score 804.5; DB 2; Length 360;
Best Local Similarity 47.7%; Pred. No. 3.4e-78;
Matches 173; Conservative 49; Mismatches 90; Indels 51; Gaps 8;
QY 11 PASAIGFEGYKRL EITFSEAPVFDPHGSLRALSRSQIDSVLDLAR----- 58
DB 6 PVSIAIGFEGYKRL EISFVEPLFADPNKGRLSLTKAQLDELGLPAEACTIVDNLNDYV 65
QY 59 -----KIVIKTCGTTKLLITIPRIELAEELSMPAAVKYSGRTFIP 103
DB 66 DSVVLSSESLFYISYKIIKTCGTTKLLITIPRIELAEELSMPAAVKYSGRTFIP 125
QY 104 QAPAPHRSESEVAVLNRYFGGLKSGGNAYVIGDAARPGQKWHIYYA---TEYPEQPMVNL 160
DB 126 QSFPHRHFSEVAVLDGYFGKLAAGSKAVIMGNDPKT-QKWHVYSASAGTVQCNDPVYL 184
QY 161 ENCMTGDLTPKASVFFKTNADGNTTCAKEMTKLSGISNIIPEMEICDFPEPCGYSNNAI 220
DB 185 ENCMTGDLNREKASVFFKT---EESAAHMYRSGIRKILPKSEICDFPEPCGYSNNAI 240
QY 221 HGSASFTHITPEDGFSYASVEVMGLDATALSVGLVKRVLGCFGPSEFSVAVTIFGGRG 280
DB 241 EGAANSTHITPEDGFTYASFESVGYDPKTNELGPLVERVLACFEPAEFESIAL----- 293
QY 281 QAGTWGK-----ELGAEAYDCNMVQEQLPGGGLIYQSFCAAEADAVASSPKSVLR-CF 333
||||| ||||||| : : : : : ||||||| |||
```

294 HADVATKLLHVCSDVKGYSLAEMSPBEPFGKGGSIYVQKF--TRTPCYCESPKVLKGCW 351

334 DGE 336

352 KEE 354

RESULT 5

AAU79674

ID AAU79674 standard; protein; 363 AA.

AC AAU79674;

XX

DT 15-JUL-2002 (first entry)

XX

DE Cucurbita ficifolia S-adenosylmethionine decarboxylase (SAMDC).

XX

KW Plant; polyamine metabolism-related enzyme; environmental stress;

KW vegetable; fruit; flower; food; agriculture; horticulture;

KW temperature stress; drought; improved growth; SAMDC;

KW S-adenosylmethionine decarboxylase; enzyme.

XX

OS Cucurbita ficifolia.

XX

PN WC200223974-A1.

XX

PD 28-MAR-2002.

XX

PF 31-AUG-2001; 2001WO-JP007521.

XX

PR 20-SEP-2000; 2000JP-00285423.

PR

PR 08-FEB-2001; 2001JP-00032627.

XX

PA (TOYO-) TOYODO RES CENT CO LTD.

XX

PI Kasukabe Y, Ihara I, Tachibana S;

XX

PI WPI; 2002-329978/36.

DR

DR N-PSDB; ABK48732.

XX

XX

PT Plant for selecting new breeds of e.g. vegetables, fruits and flowers for

PT food and decoration, comprises improved tolerance to environmental

PT stresses transferred with a plant-originated polyamine metabolism-

PT relating enzyme gene.

XX

PS Disclosure; Page 85-88; 108pp; Japanese.

XX

CC The present invention relates to the isolation of a plant derived

CC polyamine metabolism-related enzyme gene. Also described is a plant

CC having improved tolerance to environmental stresses that can stably

CC sustain an exogenous polyamine metabolism-related enzyme gene by

CC regulation of a promoter functioning in such plant, as compared to plants

CC free from the exogenous gene, or its descendants. The plant is useful in

CC selecting new breeds of e.g. vegetables, fruits and flowers for food and

CC decoration, particularly applicable in agriculture and horticulture. The

CC transgenic plants have improved tolerance to various environmental

CC stresses e.g. temperature and drought, and also have excellent growth.

CC The present sequence represents Cucurbita ficifolia S-adenosylmethionine

CC decarboxylase (SAMDC)

XX

SQ Sequence 363 AA;

Query Match 41.9%; Score 802; DB 5; Length 363;

Best Local Similarity 46.0%; Pred. No. 6.4e-78;

Matches 180; Conservative 52; Mismatches 85; Indels 74; Gaps 10;

11 PASAIFGEGYKRLITFSEAPVVDPHGSLRALSQJDSVLDLAR----- 58

4 PTAIFGEGYKRLVSEFFEGFADPRGMLRALSQAQJDEILTAECTIVDSLSNDYL 63

59 -----KIVIKTCGTTKLLTPIRILELAELSMPAAVKYSRGTFIFPGA 103

64 DSVLSESLFVVPYKFIKTCGTTKLLSIPALIKLADSLSNVKSRYTRGSGFIFPGA 123

104 QPAPHRFSFSEAVLNRYFGGLKSGGNAYVIG--DAARPGQKWHIYYAT-----EYRQPM 157

124 QSPHRFSFSEAVLDGYLAKGLHGSAYVWGSPDETR---KWHVYSACAMGSRSNPV 180

158 VNLEMCWTGLDTKASVFFKTNADGNTTCAKEMTKLSGISIIPMEMICDFDFPCGYSM 217

181 YTLEMCWTGLDKKASVFFKT---DTSSAANTENGIRKILPKSDICDFDFPCGYSM 236

218 NAIHGSASFSTIHTVPDGFSGYASYVMGLDATALSYGDLVKRVLCGFCPSSEFSAVATFG 277

237 NAIEGDAESTIHTVPDGFSGYASFAAGYELDDLCKVIGRVLACFPQSPDFVAL---- 292

278 GRQAGTWGKE-----LGAEAYDCNMVVEOELPGGILLIYQSFCAAEDAVASPKSVL- 330

293 ---HSDVVGVEDLCKLLCLDLKGYEGEKSCEMIGENGSGVIYQSFKNRGD-YASSPRSLM 348

331 RCFDGENAAPPFAKCKLANLVCLLEEXDAIBE 361

349 KC-----CWREDEADEE 360

RESULT 6

ABG75228

ID ABG75228 standard; protein; 363 AA.

XX

AC ABG75228;

XX

DT 12-FEB-2004 (first entry)

XX

DE Plant with improved organogenesis related protein SEQ ID NO: 4.

XX

KW Organogenesis; polyamine metabolism-associated gene; transgenic;

KW drug production; biodegradable plastic; enzyme production;

KW vaccine production; promoter; plant; callus.

XX

OS Cucurbita ficifolia.

XX

XX WO2003084314-A1.

PN

PD 16-OCT-2003.

XX

XX 08-APR-2003; 2003WO-JP004427.

PF

XX 08-APR-2002; 2002JP-00105583.

PR

XX (TOYO-) TOYODO RES CENT CO LTD.

XX

PA Kasukabe Y, Ihara I, Tachibana S, Matsui K, Mizutani M;

XX

PI WPI; 2003-833547/77.

DR

DR N-PSDB; ACF04931.

XX

PT Construction of plants with improved organogenesis of e.g. stem, leaf,

PT flower, fruit or seed for retaining plant-originated polyamine metabolism

PT -associated gene, applicable in producing useful substances including

PT drugs.

XX

PS Claim 7; Page 70-72; Opp; Japanese.

XX

CC The present invention relates to plants and their offspring which stably

CC retain 1 or more nucleic acid sequences for regulating polyamine dose

CC under the control of a promoter functionally in the plant and have at

CC least an improved organogenesis as compared with plants without such

CC nucleic acid sequences. The constructed plants are applicable in

CC producing useful substances including drugs, biodegradable plastics,

CC vaccines and enzymes. Such method is particularly applicable in

CC agriculture and horticulture. The present sequence is a protein shown in

CC the exemplification of the invention

XX

SQ Sequence 363 AA;

Query Match 41.9%; Score 802; DB 7; Length 363;

```
Best Local Similarity 46.0%; Pred. No. 6.4e-78;
Matches 180; Conservative 52; Mismatches 85; Indels 74; Gaps 10;

QY 11 PASAIGFEGYEKLEITFSEAPVFPVPHGSLRALSRSQIDSVLDLAR-----58
Db 4 PTAIGFEGYEKLEVSFFEPGIFADPRGMGLRALSQAQDLTLTAECTIVDSLSNDYL 63
QY 59 -----KIVIKTCGTTKLLTIPRIELABELSMPLAAVKYSRGTFFPPGA 103
Db 64 DSVLSESSLFVVPYKFIKTCGTTKLLSIPALIKLADSLSNVKSRYTRGSFIFPPGA 123
QY 104 QPAPHRSPSEEVAVLNRYFGLKSGGNAYVIG--DAARPCQKWHIYAT-----EYEPQPM 157
Db 124 QSPFHRSPSEEVAVLDGYLAKLHGSAVMGSPDETR---KWHVYSACAKMGRSRNPV 180
QY 158 VNLWCMTGLDTKKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFEPCGYSM 217
Db 181 YLLEMCMTGLDKKASVFFKTT---DTSSAAAMTENSIGIRKLPKSDICDFDFPCGYSM 236
QY 218 NAIHGSAFSTIHVTPEDGFSYASYEVNGLDATALSYGDLVKRVLCGFGPSEFSVAVTIFG 277
Db 237 NAIEGDAESTIHVTPREGFSYASFEAAGYELDDLDLCKVIGRVLACFPQSDFSVAL---292
QY 278 GRQAGTWGKE-----LGAEAYDCNMVQEQLPGGGILYQSFCAEDAVASSPKSVL- 330
Db 293 ---HSDVVGEDLDLCKLKGEGEKSCEMLGENGSVIYQSFKNRGD--YASSPRSIILM 348
QY 331 RCFDGENAAPPFAKCKLANLVCLLEEXDAIEE 361
Db 349 KC-----CWREDEADEE 360

RESULT 7
ADP90956
ID ADP90956 standard; protein; 363 AA.
AC ADP90956;
XX
XX
XX 23-SEP-2004 (first entry)
XX
XX Figleaf gourd S-adenosylmethionine decarboxylase (SAMDC) 1814 protein.
XX plant; environmental stress resistance; polyamine promoter; fat; oil;
XX cellulose; hydrocarbon; pigment; enzyme production; natural rubber;
XX pharmaceutical; figleaf gourd; S-adenosylmethionine decarboxylase;
XX SAMDC 1814; enzyme; EC 4.1.1.50.
XX
XX Cucurbita ficifolia.
XX
XX JP2004180588-A.
XX
XX 02-JUL-2004.
XX
XX 03-DEC-2002; 2002JP-00351750.
XX
XX 03-DEC-2002; 2002JP-00351750.
XX
XX (TOYO-) TOYOBO SOGO KENKYUSHO KK.
XX
XX WPI; 2004-472277/45.
XX
XX N-PSDB; ADP90955.
XX
XX Novel plant exhibiting improved environmental stress resistance and
XX having nucleic acid controlling amount of polyamines, useful for
XX obtaining substances such as fat and oil, cellulose, and natural rubber.
XX
XX Example 1; SEQ ID NO 4; 69pp; Japanese.
XX
XX The invention relates to a novel plant, or its offspring, exhibiting
XX improved environmental stress resistance and having a nucleic acid which
XX controls the amount of polyamines under the control of a promoter that
XX functions in the plant, compared with the plant which does not possess
XX the nucleotide and where the nucleotide is maintained stably within the
XX
```

```
CC plant. The polynucleotide of the invention may be useful for obtaining
CC substances such as fat and oil, cellulose, hydrocarbon, pigment, enzymes,
CC natural rubber and pharmaceutical compounds. The plant has improved
CC oxidative stress, herbicide, salt, osmotic pressure, water or low
CC temperature resistance. The current sequence is that of the figleaf gourd
CC S-adenosylmethionine decarboxylase (SAMDC) 1814 protein of the invention.
XX
XX Sequence 363 AA;
Query Match 41.9%; Score 802; DB 8; Length 363;
Best Local Similarity 46.0%; Pred. No. 6.4e-78;
Matches 180; Conservative 52; Mismatches 85; Indels 74; Gaps 10;

QY 11 PASAIGFEGYEKLEITFSEAPVFPVPHGSLRALSRSQIDSVLDLAR-----58
Db 4 PTAIGFEGYEKLEVSFFEPGIFADPRGMGLRALSQAQDLTLTAECTIVDSLSNDYL 63
QY 59 -----KIVIKTCGTTKLLTIPRIELABELSMPLAAVKYSRGTFFPPGA 103
Db 64 DSVLSESSLFVVPYKFIKTCGTTKLLSIPALIKLADSLSNVKSRYTRGSFIFPPGA 123
QY 104 QPAPHRSPSEEVAVLNRYFGLKSGGNAYVIG--DAARPCQKWHIYAT-----EYEPQPM 157
Db 124 QSPFHRSPSEEVAVLDGYLAKLHGSAVMGSPDETR---KWHVYSACAKMGRSRNPV 180
QY 158 VNLWCMTGLDTKKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFEPCGYSM 217
Db 181 YLLEMCMTGLDKKASVFFKTT---DTSSAAAMTENSIGIRKLPKSDICDFDFPCGYSM 236
QY 218 NAIHGSAFSTIHVTPEDGFSYASYEVNGLDATALSYGDLVKRVLCGFGPSEFSVAVTIFG 277
Db 237 NAIEGDAESTIHVTPREGFSYASFEAAGYELDDLDLCKVIGRVLACFPQSDFSVAL---292
QY 278 GRQAGTWGKE-----LGAEAYDCNMVQEQLPGGGILYQSFCAEDAVASSPKSVL- 330
Db 293 ---HSDVVGEDLDLCKLKGEGEKSCEMLGENGSVIYQSFKNRGD--YASSPRSIILM 348
QY 331 RCFDGENAAPPFAKCKLANLVCLLEEXDAIEE 361
Db 349 KC-----CWREDEADEE 360

RESULT 8
ADP90956
ID ADP90956 standard; protein; 363 AA.
AC ADP90956;
XX
XX
XX 18-NOV-2004 (first entry)
XX
XX Fig leaf gourd S-adenosylmethionine decarboxylase (SAMDC) protein SeqID 4.
XX transgenic; plant; productivity; polyamine metabolism; fig leaf gourd;
XX S-adenosylmethionine decarboxylase; SAMDC; enzyme.
XX
XX Cucurbita ficifolia.
XX
XX JP2004242510-A.
XX
XX 02-SEP-2004.
XX
XX 10-FEB-2003; 2003JP-00032606.
XX
XX 10-FEB-2003; 2003JP-00032606.
XX
XX (TOYO-) TOYOBO SOGO KENKYUSHO KK.
XX
XX WPI; 2004-608540/59.
XX
XX N-PSDB; ADP90955.
XX
XX Enhanced plant e.g. sweet potato, has transgenic plant with better
XX productivity and character regardless of cultivation environment compared
XX to plant without nucleic acid.
```

```

XX PS Example 1; SEQ ID NO 4; 56pp; Japanese.
XX CC This invention relates to a novel transgenic plant with improved
XX CC productivity. Specifically, it refers to transforming a plant, for
XX CC example a sweet potato, rose, sunflower, tobacco or shiitake mushroom,
XX CC with a nucleic acid molecule. This DNA molecule encoding an enzyme that
XX CC modulates polyamine metabolism such that the plant is stably maintained.
XX CC The present invention describes a method to improve the appearance of the
XX CC plant, for example the stalk, bud, flower petal or fruit, and thus
XX CC improve the commercial value of the plant. This polypeptide sequence is
XX CC the fig leaf gourd S-adenosylmethionine decarboxylase (SAMDC) protein,
XX CC encoded by a polyamine metabolism related gene of the invention.
XX Sequence 363 AA;
XX
XX Query Match 41.9%; Score 802; DB 8; Length 363;
XX Best Local Similarity 46.0%; Pred. No. 6.4e-78;
XX Matches 180; Conservative 52; Mismatches 85; Indels 74; Gaps 10;
XX
XX QY 11 PASAIGFEGYKLEITFSEAPVFPVDPHGSLRALRSQDSVLDLAR----- 58
XX DB 4 PTAIGCFEGYKLEVSFFPFGIFADPRGMLRALSKAQIDELTLAECTIVDSLSNDYL 63
XX QY 59 -----KIVIKTCGTTKLLITIPILELAELSMLAAYKYSRGTFIFPGA 103
XX DB 64 DSVLSESLFVYPYKFIITCGTTKLLISIPALIKLADSLNVSVRVTRGSFIFPGA 123
XX QY 104 QPAPHRFSFEVAVLNRYFGLKSGGNAYVIG--DAARPGQKWHIYYAT----EYPEQPM 157
XX DB 124 QSPHRFSFEVAVLDGLYAKLGLHGSAYVMGSPDETR---KHWVYSACAKMGSRSNPV 180
XX QY 158 VNLEMCMTGIDTKKASVFFKTNADGNTCAKMTKLSGISEIPEMEICDFDEPCGYSM 217
XX DB 181 YTLECMCTGLDKGKASVFFKT---DTSSAAAMTENSIRKILPKSDICDFEDPCGYSM 236
XX QY 218 NATHGSASFTHVTPEDGFYSASVEVMGLDATALSYGDLVKRVLGCFGPSEFSAVATIFG 277
XX DB 237 NALGEGDAESTHVTPEEGFSYAFEAAGYELDDLDLCKVIGRVLACFPQSDFSVAL---- 292
XX QY 278 GRGQAGTWGKE-----LGAEAYDCNNMVQELPFGGGLIYQSFCAEDAVASSPKSVL- 330
XX DB 293 --HSDVVGEDLKLCLDLKYGEGGKSCMLGENGSVIYQSFKNRGD-YASSPSRILM 348
XX QY 331 RCFDGENAAPPFAKDCKLANVLCEEXDAIEE 361
XX DB 349 KC-----CWREDADEE 360
XX
XX RESULT 9
XX AAG28816
XX ID AAG28816 standard; protein; 366 AA.
XX AC
XX AAAG28816;
XX XX
XX DT 17-OCT-2000 (first entry)
XX XX
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 34176.
XX XX
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX XX
XX OS Arabidopsis thaliana.
XX XX
XX PN EP1033405-A2.
XX XX
XX PD 06-SEP-2000.
XX XX
XX PF 25-FEB-2000; 2000EP-00301439.
XX XX
XX PR 25-FEB-1999; 99US-0121825P.
XX PR 05-MAR-1999; 99US-0123180P.
XX PR

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PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0132863P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 18-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
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PR 14-JUL-1999; 99US-0143624P.

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AAG28817
ID AAG28817 standard; protein; 215 AA.
XX AC AAG28817;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 34177.
XX DE Arabidopsis thaliana.
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
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PR 28-OCT-1999; 99US-0161920P.
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PR 29-OCT-1999; 99US-0162142P.

Query Match 20.6%; Score 393.5; DB 3; Length 184;

Best Local Similarity 46.4%; Pred. No. 6.9e-34;

Matches 90; Conservative 24; Mismatches 57; Indels 23; Gaps 6;

QY 162 MCMTGLDTKCAVFFKTNADGNNTTCAKEMTKLSGISEIIPEMICDPDPFCGYSMNAIH 221

Db 1 MCMTGLDREKAAVFKDEADKTGS---MTDNGIRKILPKSICDPEFPCGYSMNSIE 56

QY 222 GSASFSTIHTVPEDGFSYASVYVWGLDATALSYGDLVKRVLCGCPSPSEFSVAVTIFGRGQ 281

Db 57 GDAISTIHVTPEDGFSYASVYVWGLDATALSYGDLVKRVLCGCPSPSEFSVAVTIFGRGQ 113

QY 282 AGTWGKEL--GABAYDCNNMVEQL--PGGILIYQSF-----CAAEAVASPKSVLRC 332
 Db 114 ANSYKEITVDLEDYGCRTFESLGEESTVMYQTEKLGKVC-----GSFRSTLKC 166
 QY 333 FDGENAAPFAKOCK 346
 Db 167 EWSNNNSCSSEDEK 180

RESULT 14
 ADN22644
 ID ADN22644 standard; protein; 368 AA.
 AC ADN22644;
 DT 02-DEC-2004 (first entry)
 DE Bacterial polypeptide #5297.
 KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 OS Bacteria.
 XX US2003233675-A1.
 XX 18-DEC-2003.
 XX 20-FEB-2003; 2003US-00369493.
 XX 21-FEB-2002; 2002US-0360039P.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX WPI; 2004-061375/06.
 XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 PS Claim 1; SEQ ID NO 5297; 122pp; English.
 CC The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan

CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 368 AA;
 Query Match 19.7%; Score 377.5; DB 8; Length 368;
 Best Local Similarity 32.3%; Pred. No. 1.1e-31;
 Matches 108; Conservative 57; Mismatches 92; Indels 77; Gaps 16;
 QY 17 FEGYERLEITFSEAPVFDVPHGSGRLALSRSDISVLDLAR-----58
 Db 25 FEGAELLELWFCSS---IQNETRSLRIIPREIDAMLDIARCKILHSKHESIDSVLS 81
 QY 59 -----KIVIKTCGTTKLLTIPRIELEAELS--MPLAAVKYISRGTFIPGAQPAP 107
 Db 82 ESSLFISDNRVILKTCGTTLLAALPVMQLAGAYAGLDQVQSVYYSRKNFLRPDLQPSL 141
 QY 108 HRSFSEVAVLNRYFGGLKSGGNAYVIGDAARFGQKWHIY---VATEYP--EOPMVNLEM 162
 Db 142 HKNFDAEVEVLDSEFF---VDGHAYCLGLSKQ--DRWLYTFHREVEFPAHKQDHTLEI 195
 QY 163 CMTGLDTKKASVFFKTNA--DGNTTCAKEMTKLSGISBIPE--MEICDFDFEPCGYSNNAI 220
 Db 196 LMSDLDEEVLHKFTKDYAVDGNDCFMK-----AGIDKIIIPAGADVHDELDFPCGYSNNAY 250
 QY 221 HGSA--FSTIHTPDEGFSYASYEVMGLDATALSYGDLV-----KXVLGCGFSEFSVA 272
 Db 251 MNDTDQYATHVTPEKAFSPASFE-----TNODLVCLYSQTRKVLQCFRPNK--IL 299
 QY 273 VTIFGGRGAGTGWKELGAEAYDCNNMVEQLPG 306
 Db 300 MTVFA--NDISEKGDAQQOQLWD-----RELPG 325

RESULT 15
 ADN22643
 ID ADN22643 standard; protein; 368 AA.
 AC ADN22643;
 DT 02-DEC-2004 (first entry)
 DE Bacterial polypeptide #5296.
 KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 OS Bacteria.
 XX US2003233675-A1.
 XX 18-DEC-2003.
 XX 20-FEB-2003; 2003US-00369493.
 XX 21-FEB-2002; 2002US-0360039P.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 5296; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 368 AA;

Query Match 19.7%; Score 377.5; DB 8; Length 368;
Best Local Similarity 32.3%; Pred. No. 1.1e-31;
Matches 108; Conservative 57; Mismatches 92; Indels 77; Gaps 16;
QY 17 FEGYKRLKLETTSEAPVFDVPHGSLRLSRSOIDSVDLRLAR----- 58
Db 25 FEGAELLELWFCSS---TQNETRSLRIIPREIDAWLDIARCKILHSHKNEISIDSYVLS 81
QY 59 -----KIVIKTCGTTKLLTIPRIILEABELS--MPLAAYKYSRGTFFPFGQAPAP 107
Db 82 ESSLFISDNRVILKTCGTTFLAALPVMQAGAYAGLDQVQSVYSRKNFLRPDLQPSL 141
QY 108 HRSFSEVAVLNRYPGGLKSGGNAYVIGDAARPGQKWHIY---YATEYP--EOPMVNLEM 162
Db 142 HKNFDAEVEYLDSEF---VDGHAYCLGSLKQ--DRWLYTFHREVEFFPAHKQPDHTLEI 195
QY 163 CMTGLDTKASVFFKTA-DGNTTCAKEMTKLGSISEIPE-MEICDFDFPCGYSNNAI 220
Db 196 LMSDLDEEVHLKFTKYAVDGNDFWR-----AGIDKIIPAGADVHDELDFPCGYSNNAY 250
QY 221 HGSA--FSTIHTVPEDFGSYASVEVMGLDATALSYGDLV-----KRVLCGFCGSEFSVA 272
Db 251 MNDTDQYATHVTPKAFSEFSE-----TNQDLVCLYSQTRKVLQCFRPNK--IL 299
QY 273 VTIFGGRGQAGTWGKELGABAYDCNNMVEQLPG 306
Db 300 MTVFA--NDISEKGDQAQQQLWD-----RELPG 325

Search completed: May 11, 2005, 22:47:50
Job time : 95.8969 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2005, 22:38:57 ; Search time 94.5017 Seconds
(without alignments)
2167.492 Million cell updates/sec

Title: US-10-732-923-408

Perfect score: 2097

Sequence: 1 MAVLSAADSPVSAIGFEGY.....LLCWEEADAMBEKAGVLDE 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2097	100.0	400	1	DCAM MAIZE
2	1715	81.8	398	1	DCAM ORYZA
3	1715	81.8	398	2	Q7XT83
4	1682.5	80.2	393	1	DCAM HORCH
5	1663	79.3	392	2	Q92BJ1
6	1632	77.8	395	2	Q6K9B8
7	1632	77.8	395	2	Q9SC67
8	1357	64.7	392	2	Q6FAN6
9	1338.5	63.8	370	2	Q84LA2
10	1300	62.0	369	2	Q944U3
11	1290	61.5	319	2	Q9F8M2
12	1090	47.7	358	2	Q7XZQ9
13	980	46.7	357	1	DCAM CATRO
14	969	46.2	361	1	DCAM NICSY
15	969	46.2	361	1	DCAM TOBAC
16	969	46.2	362	1	DCAM DATST
17	968.5	46.2	374	2	Q852S8
18	966	46.1	358	2	Q852S9
19	965.5	46.0	353	1	DCAM VICFA
20	962	45.9	362	1	DCAM IPONI
21	961.5	45.9	363	1	DCAM SPIOL
22	960.5	45.8	361	2	Q8LKJ7
23	960	45.8	362	1	DCAM IPOBA
24	954	45.5	377	1	DCA2 DIACA
25	952	45.4	349	2	Q9LSU6
26	950	45.3	354	2	Q8W3Y2
27	946.5	45.1	353	1	DCAM PEA
28	944	45.0	381	1	DCA1 DIACA
29	941.5	44.9	360	1	DCAM SOLTU
30	919.5	43.8	355	2	Q8S3F8
31	915.5	43.7	361	2	Q6RUQ3

RESULT 1

ID	DCAM MAIZE	STANDARD	PRT	400 AA
AC	Q24575			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)			
DE	(SambDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain].			
GN	Name=SAMDC;			
OS	Zea mays (Maize).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC	PACCAD clade; Panicoideae; Andropogoneae; Zea.			
OX	NCBI_TaxID=4577;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Michael A.J.;			
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.			
CC	-1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (5-deoxy-5-adenosyl) (3-aminopropyl)-methylsulfonium salt + CO(2).			
CC	-1- COPACTOR: Pyruvyl group (By similarity).			
CC	-1- PATHWAY: Decarboxylation of S-adenosylmethionine provides the aminopropyl moiety required for spermidine and spermine biosynthesis from putrescine.			
CC	-1- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.			
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CC	EMBL: Y07767; CAA69075.1; -			
DR	PIR: T03947; T03947.			
DR	HSSP: P17707; LJEN.			
DR	InterPro: IPR001985; SAM decarbox.			
DR	Pfam: PF01536; SAM decarbox; 1.			
DR	ProDom: PD002379; SAM decarbox; 1.			
DR	TIGRFAMs: TIGR00535; SAM DCase; 1.			
DR	PROSITE: PS01336; ADOMETDC; 1.			
KW	Decarboxylase; Lyase; Pyruvate; Spermidine biosynthesis; Zymogen.			
FT	CHAIN 1 77			
FT	S-adenosylmethionine decarboxylase beta chain (By similarity).			
FT	CHAIN 78 400			
FT	S-adenosylmethionine decarboxylase alpha chain (By similarity).			
FT	SITE 77 78			
FT	Cleavage (nonhydrolytic) (By similarity).			
FT	MOD_RES 78 78			
FT	Pyruvic acid (Ser) (By similarity).			
FT	ACT_SITE 18 18			
FT	By similarity.			
FT	ACT_SITE 21 21			
FT	By similarity.			
FT	ACT_SITE 92 92			
FT	By similarity.			

Q9axe3 daucus caro
Q96286 arabidopsis
Q65354 helianthus
Q6azs4 brassica ju
Q94005 arabidopsis
Q49972 brassica ju
Q96719 arabidopsis
Q96dm8 brassica ju
Q6qj69 brassica ju
Q42613 brassica ju
Q6kc47 prunus pers
Q9sc65 oryza sativ
Q8vx33 vitis vinif
Q76kv7 pisum sativ

ALIGNMENTS

SQ SEQUENCE 400 AA; 43515 MW; 1B2445775P55714A CRC64;

Query Match 100.0%; Score 2097; DB 1; Length 400;
 Best Local Similarity 100.0%; Pred. No. 9.6e-170;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAVLSAADASPVSAIGFEGYKRELEITFSEAPVDPHGRLALSGRAQIDSVLDLART 60
 DB 1 MAVLSAADASPVSAIGFEGYKRELEITFSEAPVDPHGRLALSGRAQIDSVLDLART 60

QY 61 IVSELSNKPDSYLVSESSIFLYPLKIVIKTCCTTKLLLTIPRILELAELSPLAAVKY 120
 DB 61 IVSELSNKPDSYLVSESSIFLYPLKIVIKTCCTTKLLLTIPRILELAELSPLAAVKY 120

QY 121 SRTGTFPGAQAPAPHRFSFEVAAALNRYFGGLKSGGNVYIGDPAPRGQKWHVYATEYP 180
 DB 121 SRTGTFPGAQAPAPHRFSFEVAAALNRYFGGLKSGGNVYIGDPAPRGQKWHVYATEYP 180

QY 181 EQPMVNLWCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFEPC 240
 DB 181 EQPMVNLWCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFEPC 240

QY 241 GYSMNAIHGSAFSTIHTVTPEDGFSYASYEVMGLDATALSYGDLVKRVLRCFGSSEFSVAV 300
 DB 241 GYSMNAIHGSAFSTIHTVTPEDGFSYASYEVMGLDATALSYGDLVKRVLRCFGSSEFSVAV 300

QY 301 TIFGGRGHAGTWKALGAEVYDNNVVEOELPGGLLVYQSFCAAEEDAVATSPKSVFHC 360
 DB 301 TIFGGRGHAGTWKALGAEVYDNNVVEOELPGGLLVYQSFCAAEEDAVATSPKSVFHC 360

QY 361 DGENVESAPPPMKDYKLANLLCWEEBDAAMEEKAGVLDE 400
 DB 361 DGENVESAPPPMKDYKLANLLCWEEBDAAMEEKAGVLDE 400

RESULT 2

DCAM_ORYSA STANDARD; PRT; 398 AA.

AC 024215; 081269;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
 DE (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain].
 GN Name=SAMDC;
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoideae; Oryzae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Japonica / Nipponbare;
 RX MEDLINE=21066059; PubMed=11139406; DOI=10.1042/0264-6021.3530403;
 RA Franceschetti M., Hanfrey C., Scaramagli S., Torrigiani P., Bagni N.,
 RA Michael A.J.;
 RA "Characterization of monocot and dicot plant S-adenosyl-L-methionine
 RT decarboxylase gene families including identification in the mRNA of a
 RT highly conserved pair of upstream overlapping open reading frames.";
 RL Biochem. J. 353:403-409 (2001).
 RN [2]

SEQUENCE FROM N.A.
 RA Li Z.Y., Chen S.Y.;
 RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (5-deoxy-5-adenosyl) (3-aminopropyl)-methylsulfonium salt + CO(2).
 CC -1- COFACTOR: Pyruvoyl group.
 CC -1- PATHWAY: Decarboxylation of S-adenosylmethionine provides the
 CC aminopropyl moiety required for spermidine and spermine
 CC biosynthesis from putrescine.
 CC -1- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.

CC -----

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CC EMBL; Y07766; CAA69074.2; -;
 CC EMBL; AF067194; AAC79990.1; -;
 CC HSSP; P17707; I172.
 CC Gramene; O24215; -;
 CC InterPro; IPR001985; SAM decarbox.
 CC Pfam; PF01536; SAM decarbox; 1.
 CC ProDom; PD002379; SAM decarbox; 1.
 CC TIGRFAMs; TIGR00535; SAM DCase; 1.
 CC PROSITE; PS01336; ADOMETDC; 1.
 KW Decarboxylase; Lyase; Pyruvate; Spermidine biosynthesis; Zymogen.
 FT CHAIN 1 77 S-adenosylmethionine decarboxylase beta
 FT chain (By similarity).
 FT CHAIN 78 398 S-adenosylmethionine decarboxylase alpha
 FT chain (By similarity).
 FT SITE 77 78 Pyruvic acid (Ser) (By similarity).
 FT MOD_RES 78 78 Cleavage (nonhydrolytic) (By similarity).
 FT ACT_SITE 18 18 By similarity.
 FT ACT_SITE 21 21 By similarity.
 FT ACT_SITE 92 92 By similarity.
 FT CONFLICT 250 250 S -> L (in Ref. 2).
 SQ SEQUENCE 398 AA; 43283 MW; BC24F359962F8655 CRC64;

Query Match 81.8%; Score 1715; DB 1; Length 398;
 Best Local Similarity 83.3%; Pred. No. 3e-137;
 Matches 335; Conservative 21; Mismatches 40; Indels 6; Gaps 4;

QY 1 MAVLSAADASPVSAIGFEGYKRELEITFSEAPVDPHGRLALSGRAQIDSVLDLART 60
 DB 1 MGVLSAADPPVSAIGFEGYKRELEITFSEAPVDPHGRLALSGRAQIDSVLDLART 60

QY 61 IVSELSNKPDSYLVSESSIFLYPLKIVIKTCCTTKLLLTIPRILELAELSPLAAVKY 120
 DB 61 IVSELSNKPDSYLVSESSIFLYPLKIVIKTCCTTKLLLTIPRILELAELSPLAAVKY 120

QY 121 SRTGTFPGAQAPAPHRFSFEVAAALNRYFGGLKSGGNVYIGDPAPRGQKWHVYATEYP 180
 DB 121 SRTGTFPGAQAPAPHRFSFEVAAALNRYFGGLKSGGNVYIGDPAPRGQKWHVYATEYP 180

QY 181 EQPMVNLWCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFEPC 240
 DB 181 EQPMVNLWCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFEPC 240

QY 241 GYSMNAIHGSAFSTIHTVTPEDGFSYASYEVMGLDATALSYGDLVKRVLRCFGSSEFSVAV 300
 DB 241 GYSMNAIHGSAFSTIHTVTPEDGFSYASYEVMGLDATALSYGDLVKRVLRCFGSSEFSVAV 300

QY 301 TIFGGRGHAGTWKALGAEVYDNNVVEOELPGGLLVYQSFCAAEEDAVATSPKSVF 358
 DB 301 TIFGGRGHAGTWKALGAEVYDNNVVEOELPGGLLVYQSFCAAEEDAVATSPKSVF 358

QY 359 CFGENVESAPPPMKDYKLANLLCWEEBDAAMEEKAGVLDE 400
 DB 361 CFEAENMVN-PAPVKEG-KLGNLLPWGE--DALEENDGVFDE 398

RESULT 3

Q7XT83 PRELIMINARY; PRT; 398 AA.

AC Q7XT83; Q7XUL0;
 DT 01-OCT-2003 (T-EMBLrel. 25, Created)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE OSJNBa0029H02.2 protein (OSJNBa0067K08.23 protein).
 GN Names=OSJNBa0029H02.2; Synonyms=OSJNBa0067K08.23;
 OS Oryza sativa (japonica cultivar-group).

25-OCT-2004 (Rel. 45, Last annotation update)
S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
DE (Samdc) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-
DE adenosylmethionine decarboxylase beta chain].
GN Name=SAMDC;
OS Hordeum chilense (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=15565;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=leaf;
MSLINES=96270379; PubMed=8639739;
RA Dresselhaus T., Barcelo P., Hagel C., Loerz H., Humbeck K.;
RT "Isolation and characterization of a Tritordeum cDNA encoding S-
RT adenosylmethionine decarboxylase that is circadian-clock-regulated.";
RL Plant Mol. Biol. 30:1021-1033(1996).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S-deoxy-S-
CC adenosyl) (3-aminopropyl)-methylsulfonium salt + CO(2).
CC -1- COFACTOR: Pyruvoyl group.
CC -1- PATHWAY: Decarboxylation of S-adenosylmethionine provides the
CC aminopropyl moiety required for spermidine and spermine
CC biosynthesis from putrescine.
CC -1- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.

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CC or send an email to license@ebi.ac.uk).

DR EMBL: X83881; CAA58762.1; --
DR PR: S69191; S69191.
DR RSP: P17707; IJEN.
DR InterPro: IPR001985; SAM_decarbox.
DR Pfam: PF01536; SAM_decarbox; 1.
DR ProDom: PD002379; SAM_decarbox; 1.
DR TIGRfam: TIGR00535; SAM_DCcase; 1.
DR PROSITE: PS01336; ADOMETDC; 1.
KW Decarboxylase; Lyase; Pyruvate; Spermidine biosynthesis; Zymogen.
FT CHAIN 1 70 S-adenosylmethionine decarboxylase beta
FT FT chain (By similarity).
FT CHAIN 71 393 S-adenosylmethionine decarboxylase alpha
FT FT chain (By similarity).
FT SITE 70 71 Cleavage (nonhydrolytic) (By similarity).
FT MOD_RES 71 71 Pyruvic acid (Ser) (By similarity).
FT ACT_SITE 11 11 By similarity.
FT ACT_SITE 14 14 By similarity.
FT ACT_SITE 85 85 By similarity.
FT ACT_SITE 85 85 By similarity.
SQ SEQUENCE 393 AA; 42895 MW; 6CDIAA94792AF6CB CRC64;
Query Match 80.2%; Score 1682.5; DB 1; Length 393;
Best Local Similarity 82.7%; Pred. No. 1.7e-134;
Matches 324; Conservative 25; Mismatches 38; Indels 5; Gaps 3;
Qy 9 ASPVSAIGFGYEGKRLIEITFSEAPVFDPHGRGRLASRAQIDSVLDLACTIVSELSNK 68
Db 2 AAPVSAIGFGYEGKRLIEITFSEASIFADPHGRGRLASRAQIDSVLDLACTIVSELSNK 61
Qy 69 DFDYSVLSESSLFIYPLKIVIKTCGTTKLLTTIPRIELEAELSMPLAAVKYSRGTFFP 128
Db 62 DFDYSVLSESSLFIYQKIVIKTCGTTMLTTIPRIELEAELCMPLAAVKYSRGMEIFP 121
Qy 129 GAQPAPHRFSSEVAALNRYFGLKSGGNAYVIGDPAKPGQKWHVFYATPEPQPMWNL 188
Db 122 GAQPAPHRFSSEVDVNLNRYFGLHNSGNNAYVIGDPAKPGQKWHVYATPEPQPMVTL 181
Qy 189 MCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISIIPMEICDFDPFCGYSNNAIH 248
Db 182 MCMTGLDKTKASVFFKTHADGHVSCAKEMTKLSGISIDIIPEMEVCDPFPFCGYSNNAIN 241

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QY 249 GSAFSTHVTPEGFSVASYEVWGLDATALSYGDLVKRVLRCFSPSEFSVAVTIFGGRGH 308
Db 242 GSAFSTHVTPEGFSVASYEVWGLDATALSYGDLVKRVLRCFSPSEFSVAVTIFGGRGH 301
QY 309 AGTWKALGAEVYDCNNVWQELPGGGLLYQSFCAEDAV--ATSPKSVFHCFCGDNVE 366
Db 302 AATWGGKLDAAEDCNVWQELPGGGLLYQSFCAEDAV--ATSPKSVFHCFCGDNVE 359
QY 367 SAPPMKKDYKLANLLCWEEEDAMEEKA 398
Db 360 SG-HPLVKEGKLANLLAWRAEEDSLEBGTAL 390

RESULT 5
Q9ZPJ1 ID Q9ZPJ1 PRELIMINARY; PRT; 392 AA.
AC Q9ZPJ1
DT 01-MAY-1999 (T-EMBLrel. 10, Created)
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE S-adenosylmethionine decarboxylase.
OS Triticum aestivum (wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RA Li Z.Y., Chen S.Y.;
RT "Isolation and characterization of a salt and drought-inducible gene
RT for S-adenosylmethionine decarboxylase from wheat (Triticum aestivum
RT L.).";
RL J. Plant Physiol. 156:386-393 (2000).
DR EMBL; AF117660; AAD17232.1; -.
DR HSP: P17707; IJEN
DR GO: GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
DR GO: GO:0008295; P:spermidine biosynthesis; IEA.
DR GO: GO:0006597; P:spermine biosynthesis; IEA.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRfam; TIGR00535; SAM DCase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
SQ SEQUENCE 392 AA; 42854 MW; C761765631C2B91F CRC64;

Query Match 79.3%; Score 1663; DB 2; Length 392;
Best Local Similarity 81.7%; Pred. No. 7.8e-133;
Matches 318; Conservative 26; Mismatches 41; Indels 4; Gaps 2;

QY 9 ASPVSAIGFEGYEKRLKLEITFSEAPVFDPHGRGLRALSRQAIDSVDLRLACTIVSELSTK 61
Db 2 AAPTSAIGFEGYEKRLKLEITFSEAPVFDPHGRGLRALSRQAIDSVDLRLACTIVSELSTK 61
QY 69 DFDYVLSSESLFIYPLKIVIKTCGTTKLLTIPRILELAELSMPLEAAVKYRGFIFF 128
Db 62 DFDYVLSSESLFIYPLKIVIKTCGTTKLLTIPRILELAELSMPLEAAVKYRGFIFF 121
QY 129 GAOPAPHRSPSEVAALNRYFGGLKSGGNAYVIGDPAKQKWHVYFATEYPPQMVNLE 188
Db 122 GAOPAPHRSPSEVAALNRYFGGLKSGGNAYVIGDPAKQKWHVYFATEYPPQMVNLE 181
QY 189 MCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDPDFPCGYSMAIH 248
Db 182 MCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDPDFPCGYSMAIH 241
QY 249 GSAFSTHVTPEGFSVASYEVWGLDATALSYGDLVKRVLRCFSPSEFSVAVTIFGGRGH 308
Db 242 GSAFSTHVTPEGFSVASYEVWGLDATALSYGDLVKRVLRCFSPSEFSVAVTIFGGRGH 301
QY 309 AGTWKALGAEVYDCNNVWQELPGGGLLYQSFCAEDAV--ATSPKSVFHCFCGDNVE 366
Db 302 AATWGGKLDAAEDCNVWQELPGGGLLYQSFCAEDAV--ATSPKSVFHCFCGDNVE 361

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QY 367 SAPPMKKDYKLANLLCWEEEDAMEEKA 395
Db 362 S-HPLVKEGKLANLLAWRAEEDSLEBGA 388

RESULT 6
Q6K9B8 ID Q6K9B8 PRELIMINARY; PRT; 395 AA.
AC Q6K9B8
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE S-adenosylmethionine decarboxylase 2.
OS Oryza sativa (japonica cultivar-group).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004063; BAD19232.1; -.
DR EMBL; AP005286; BAD19677.1; -.
DR GO: GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
DR GO: GO:0008295; P:spermidine biosynthesis; IEA.
DR GO: GO:0006597; P:spermine biosynthesis; IEA.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRfam; TIGR00535; SAM DCase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
SQ SEQUENCE 395 AA; 43152 MW; 49C9BC56F20FE540 CRC64;

Query Match 77.8%; Score 1632; DB 2; Length 395;
Best Local Similarity 79.3%; Pred. No. 3.4e-130;
Matches 314; Conservative 26; Mismatches 46; Indels 10; Gaps 2;

QY 1 MAVLSAADASPVSAIGFEGYEKRLKLEITFSEAPVFDPHGRGLRALSRQAIDSVDLRLACT 60
Db 1 MAVLSAADASPVSAIGFEGYEKRLKLEITFSEAPVFDPHGRGLRALSRQAIDSVDLRLACT 60
QY 61 IVSELSNKPDSVLSSESLFIYPLKIVIKTCGTTKLLTIPRILELAELSMPLEAAVKY 120
Db 61 IVSELSNKPDSVLSSESLFIYPLKIVIKTCGTTKLLTIPRILELAELSMPLEAAVKY 120
QY 121 SRTGTFIPGAQAPHRSPSEVAALNRYFGGLKSGGNAYVIGDPAKQKWHVYFATEYPP 180
Db 121 SRTGTFIPGAQAPHRSPSEVAALNRYFGGLKSGGNAYVIGDPAKQKWHVYFATEYPP 180
QY 181 EQPMVNLKMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDPDFPC 240
Db 181 EQPMVNLKMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDPDFPC 240
QY 241 GYSMAIHGSAFSTHVTPEGFSVASYEVWGLDATALSYGDLVKRVLRCFSPSEFSVA 300
Db 241 GYSMAIHGSAFSTHVTPEGFSVASYEVWGLDATALSYGDLVKRVLRCFSPSEFSVA 300
QY 301 TIFGGRGHAGTWKALGAEVYDCNNVWQELPGGGLLYQSFCAEDAVATSPKSVFHC 360
Db 301 TIFGGRGHAGTWKALGAEVYDCNNVWQELPGGGLLYQSFCAEDAVATSPKSVFHC 360
QY 361 DGNVTSAPPMKKDYKLANLLCWEEEDAMEEKA 396
Db 361 ADENKTEKAG-----MEALYWD-----DAVEIDG 386

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RESULT 7
Q9SC67 PRELIMINARY; PRT; 395 AA.

AC Q9SC67 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE S-adenosylmethionine decarboxylase 2 (EC 4.1.1.50).
GN Name=adomc2;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzaceae; Oryza.
NCBI_TaxID=4530;
[1]
SEQUENCE FROM N.A.
RP MEDLINE=21066059; PubMed=11139406; DOI=10.1042/0264-6021.3530403;
RA Franceschetti M., Hanfrey C., Scaramagli S., Torrigiani P., Bagni N.,
RA Michael A.J.;
RT "Characterization of monocot and dicot plant S-adenosyl-methionine
RT decarboxylase gene families including identification in the mRNA of a
RT highly conserved pair of upstream overlapping open reading frames.",
RL Biochem. J. 353:403-409 (2001).
DR EMBL; AJ251899; CAB64600.1; -.
DR HSP; P17707; IJEN.
DR Gramene; Q9SC67; -.
DR GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
DR GO:0016829; F:lyase activity; IEA.
DR GO:0008295; P:spermidine biosynthesis; IEA.
DR GO:0006597; P:spermine biosynthesis; IEA.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR TrProDom; PD002379; SAM decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM_DCase; 1.
DR PROSITE; PS01336; ADOMETC; 1.
DR Lyase.
SQ SEQUENCE 395 AA; 43152 MW; 49C9BC56F20F8540 CRC64;

Query Match 77.8%; Score 1632; DB 2; Length 395;
Best Local Similarity 79.3%; Pred. No. 3.4e-130;
Matches 314; Conservative 26; Mismatches 46; Indels 10; Gaps 2;

Qy 1 MAVLSAADSPVSAIGFEGYEKRLITFSEAPVFDVPHGRGLRALSRQAIDSVLDLARCT 60
Db 1 MAVLSVADSPVSAIGFEGYEKRLITFSEAPVFDVPHGRGLRALSRQAIDSVLDLARCT 60
Qy 61 IVSELSNKDFDSVYLSSESLFIYPLKIVTKTCTGTTKLLITPRILEAEELSMPAAVKY 120
Db 61 IVSELSNEVDFSIVYLSSESLFVYPIKIVTKTCTGTTKLLAIIPRILEAEELSMPLEAVKY 120
Qy 121 SRGTFIPGQAOPAPHRSPFSEEAALNRYFGGLKSGNAVYIGDPAKQKWHVFATYRP 180
Db 121 SRGTFIPPEAQSPHKNFSEEAALNRYFGGLKSGNAVYIGDPAKQKWHVYATQHP 180
Qy 181 EQPMVNLKMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDFDEPCC 240
Db 181 EQPVVTLKMTGLDKKASVFFKTSADGHTTVAKEMTKLSGISDIPEMEVCFDPEPC 240
Qy 241 GYSNNAIHGSAFTIHTVTPEDGFSYASYEVNGLDATALSYGDLVKRVLCRCGPSEFSVAV 300
Db 241 GYSNNAIHGSAFTIHTVTPEDGFSYASYEVNGLDATALSYGDLVKRVLCRCGPSEFSVAV 300
Qy 301 TIFGGRGHAGTGWKALGAEEVDCNNVVEQLPGGLLVYQSFCAEADAVATSPKSVHCF 360
Db 301 TIFGGRNHAGTWAKGLDVGNYSNNVVEQLPGGLLVYQSFATATATSPKSVHCF 360
Qy 361 DGENVESAPPPMKDYKLANLLCWEEDADAMEKAG 396
Db 361 ADENTKAGK-----MEALYWD--DAVEIDG 386

RESULT 8
Q6F4N6 PRELIMINARY; PRT; 392 AA.

AC Q6F4N6 (TREMELrel. 28, Created)
DT 25-OCT-2004 (TREMELrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMELrel. 28, Last annotation update)
DE S-adenosylmethionine decarboxylase.
GN Name=SANDCI; Synonyms=P0418B08.27-1;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzaceae; Oryza.
NCBI_TaxID=39947;
[1]
SEQUENCE FROM N.A.
RP PubMed=15215597;
RA Yamaguchi T., Nakayama K., Hayashi T., Yazaki J., Kishimoto N.,
RA Kikuchi S., Koike S.;
RT "cDNA Microarray Analysis of Rice Anther Genes under Chilling Stress
RT at the Microsporogenesis Stage Revealed Two Genes with DNA Transposon
RT Castaway in the 5'-Flanking Region.",
RL Biosci. Biotechnol. Biochem. 68:1315-1323 (2004).
RN [2]
SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, PAC
RT clone:P0418B08.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB122089; BAD26704.1; -.
DR EMBL; AP005420; BAD33432.1; -.
DR GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
DR GO:0008295; P:spermidine biosynthesis; IEA.
DR GO:0006597; P:spermine biosynthesis; IEA.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR TrProDom; PD002379; SAM decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM_DCase; 1.
DR PROSITE; PS01336; ADOMETC; 1.
SQ SEQUENCE 392 AA; 42717 MW; 0DF1F61522C38FE3 CRC64;

Query Match 64.7%; Score 1357; DB 2; Length 392;
Best Local Similarity 67.6%; Pred. No. 8.4e-107;
Matches 267; Conservative 47; Mismatches 71; Indels 10; Gaps 5;

Qy 4 LSAAD---ASPVSAIGFEGYEKRLITFSEAPVFDVPHGRGLRALSRQAIDSVLDLARCT 60
Db 3 MSLADSWGSPASPIGFEGYEKRLITLSDAPVFDVPHGRGLRALSRQAIDSVLDLARCT 62
Qy 61 IVSELSNKDFDSVYLSSESLFIYPLKIVTKTCTGTTKLLITPRILEAEELSMPAAVKY 120
Db 63 IVSHLSNKHFDVYLSSESLFVYPIKIVTKTCTGTTKLLSIPRILEAEELSMPVLSVKY 122
Qy 121 SRGTFIPGQAOPAPHRSPFSEEAALNRYFGGLKSGNAVYIGDPAKQKWHVFATYRP 180
Db 123 SRGMFIPGQAOPSPHRSPFSEEAALNRYFGGLKSGNAVYIGDPAKQKWHVYATYRP 182
Qy 181 EQPMVNLKMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDFDEPCC 240
Db 183 EQPMVTLKMTGLDKKAAEVFFKDTSDGSCSSAKEMTFSGISIIPEMEICDFDEPCC 242
Qy 241 GYSNNAIHGSAFTIHTVTPEDGFSYASYEVNGLDATALSYGDLVKRVLCRCGPSEFSVAV 300
Db 243 GYSNNGIYGPVSTIHTVTPEDGFSYASYEVNGLDATALSYGDLVKRVLCRCGPSEFSVAV 302
Qy 301 TIFGGRGHAGTGWKALGAEEVDCNNVVEQLPGGLLVYQSFCAEADAVATSPKSVHCF 360
Db 303 TIFGGRGHAGTGWKALGAEEVDCNNVVEQLPGGLLVYQSFCAEADAVATSPKSVHCF 360
Qy 361 DGENVESAPPPMKDYKLANLLCWEEDADAMEKAG 395
Db 359 DGNWSDGA-EMVAKSKEMS--VCWEGEKAANKKDA 390

RESULT 9

Q6F4N6

```

Q84LA2
ID Q84LA2 PRELIMINARY; PRT; 370 AA.
AC Q84LA2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE S-adenosylmethionine decarboxylase.
GN Names=Samdc;
OS Narcissus pseudonarcissus (Daffodil).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;
OC Narcissus.
OX NCBI_TaxID=39639;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=4-day old flower tepals;
RA Gookin T.E., Cabauatan E.V., Hunter D.A., Reid M.S.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY232672; AA043186.1; -.
DR HSSP; P17707; 1JEN
DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
DR GO; GO:0008295; P:spermidine biosynthesis; IEA.
DR GO; GO:0006597; P:spermine biosynthesis; IEA.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM_DCase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
SQ SEQUENCE 370 AA; 40680 MW; 36F619BA4806F70F CRC64;

Query Match 63.8%; Score 1338.5; DB 2; Length 370;
Best Local Similarity 69.1%; Pred. No. 2.9e-105;
Matches 250; Conservative 47; Mismatches 64; Indels 1; Gaps 1;

QY 13 SAIGFEGYEKRLRITSEAPVFDVPHGRGLRALSRQIDSILDLARCTIVSELSNKKDFDS 72
DB 7 SPIGFEGYEKRLRITSEAPVFDVPHGRGLRALSRQIDSILDLARCTIVSELSNKKDFDS 66

QY 73 YVLSSESLFYPLKIVIKTCGTTKLLTIPRIELEAEELSMPLAAVKYSGRTIFPGAQP 132
DB 67 YVLSSESLFYPLKIVIKTCGTTKLLTIPRIELEAEELSMPLAAVKYSGRTIFPGAQP 126

QY 133 AHRSESEVAALNRVFGGLKSGNAVIGDPPARPGOKWHVFYATEVPEOPMWNLEMCMT 192
DB 127 TPRNFESEVSLDHFEGNLASGNAYIGDPPSPRNWHIYATQKPELPTVTLEMCMT 186

QY 193 GLDKKACVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDFDFPCGYSMNAIHGSAF 252
DB 187 GLDSEKASIFFNSPGNANNAQSKMTKLSGISNIIPEMEICDFDFPCGYSMNAICGSAH 246

QY 253 STIHVTPEDGFSYASVEVMGLDATALSYGLVLRVLCRCPSEFSFSAVATIFGGRGHAGTW 312
DB 247 STIHVTPEDGSSYASVEAMGFNPAELDFGLVVERVLECFGDFSAVATIFGGRGQAGSW 306

QY 313 GKALGAEVYDCNNMVEQELPGGGLLVYQSFCAAEADVATSPKSVFHCFCGDEVESAPPPM 372
DB 307 GREVDSYGFRCVDLVEQELAGGLLMTQSFAGVGRMG-SPRSTLHCWDGEEIEEKKAE 365

QY 373 KK 374
DB 366 KK 367

RESULT 10
Q944U3
ID Q944U3 PRELIMINARY; PRT; 369 AA.
AC Q944U3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE S-adenosyl-L-methionine decarboxylase.
GN Names=Samdc;
OS Dendrobium crumenatum (Tropical pigeon orchid).

QY 13 SAIGFEGYEKRLRITSEAPVFDVPHGRGLRALSRQIDSILDLARCTIVSELSNKKDFDS 72
DB 7 SPIGFEGYEKRLRITSEAPVFDVPHGRGLRALSRQIDSILDLARCTIVSELSNKKDFDS 66

QY 73 YVLSSESLFYPLKIVIKTCGTTKLLTIPRIELEAEELSMPLAAVKYSGRTIFPGAQP 132
DB 67 YVLSSESLFYPLKIVIKTCGTTKLLTIPRIELEAEELSMPLAAVKYSGRTIFPGAQP 126

QY 133 AHRSESEVAALNRVFGGLKSGNAVIGDPPARPGOKWHVFYATEVPEOPMWNLEMCMT 192
DB 127 TPRNFESEVSLDHFEGNLASGNAYIGDPPSPRNWHIYATQKPELPTVTLEMCMT 186

QY 193 GLDKKACVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDFDFPCGYSMNAIHGSAF 252
DB 187 GLDSEKASIFFNSPGNANNAQSKMTKLSGISNIIPEMEICDFDFPCGYSMNAICGSAH 246

QY 253 STIHVTPEDGFSYASVEVMGLDATALSYGLVLRVLCRCPSEFSFSAVATIFGGRGHAGTW 312
DB 247 STIHVTPEDGSSYASVEAMGFNPAELDFGLVVERVLECFGDFSAVATIFGGRGQAGSW 306

QY 313 GKALGAEVYDCNNMVEQELPGGGLLVYQSFCAAEADVATSPKSVFHCFCGDEVESAPPPM 372
DB 307 GREVDSYGFRCVDLVEQELAGGLLMTQSFAGVGRMG-SPRSTLHCWDGEEIEEKKAE 365

QY 373 KK 374
DB 366 KK 367

RESULT 11
Q9FSM2
ID Q9FSM2 PRELIMINARY; PRT; 319 AA.
AC Q9FSM2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE S-adenosylmethionine decarboxylase.
GN Names=H071106.28;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Han B., Feng Q., Mu J., Zhou B., Chen Z.H., Li Y., Zhu J.J.,
RA Tang Y.S., Zhao Q., Liu Y.L., Huang Y.C., Yu Z., Fan D.L., Chen L.,
RA Wang Q.J., Zhang L., Lu Y.Q., Yu S.L., Zhu J., Liu X.H., Hu X.,

QY 13 SAIGFEGYEKRLRITSEAPVFDVPHGRGLRALSRQIDSILDLARCTIVSELSNKKDFDS 72
DB 4 SPIGFEGYEKRLRITSEAPVFDVPHGRGLRALSRQIDSILDLARCTIVSELSNKKDFDS 63

QY 73 YVLSSESLFYPLKIVIKTCGTTKLLTIPRIELEAEELSMPLAAVKYSGRTIFPGAQP 132
DB 64 YVLSSESLFYPLKIVIKTCGTTKLLTIPRIELEAEELSMPLAAVKYSGRTIFPGAQP 123

QY 133 AHRSESEVAALNRVFGGLKSGNAVIGDPPARPGOKWHVFYATEVPEOPMWNLEMCMT 192
DB 124 AHRSESEVAALNRVFGGLKSGNAVIGDPPARPGOKWHVFYATEVPEOPMWNLEMCMT 183

QY 193 GLDKKACVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDFDFPCGYSMNAIHGSAF 252
DB 184 GLNTEKASIFFNSVPRHESKAKEMTKRSIGCIDIIPEMKICDFDFPCGYSMNKKQAL 243

QY 253 STIHVTPEDGFSYASVEVMGLDATALSYGLVLRVLCRCPSEFSFSAVATIFGGRGHAGTW 312
DB 244 STIHVTPEDGFSYASVEAMGFNPAELDFGLVVERVLECFGDFSAVATIFGGRGQAGSW 303

QY 313 GKALGAEVYDCNNMVEQELPGGGLLVYQSFCAAEADVATSPKSVFHCFCGDEVESAPPPM 372
DB 304 GKQVSYNGYCNKLVQDLSGGGLLVYQSFKASSDGS-SPRSI----- 346

QY 373 KDYKLANLLCWEAEADAMEEKAGV 397
DB 347 -----LYCWEAEAEED-EEENG 362

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RA Lei H.Y., Zhang Y.J., Wang R., Li C., Lu Y., Chen X.C., Zhang Y.,
 RA Hu H., Jia P.X., Li T., Qian Y.M., Ying K., Hong G.P.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL442115; CAC09522.1; -
 DR HSSP; P17707; I178.
 DR Gramene; Q9FSM2; -
 DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
 DR GO; GO:0008295; P:spermidine biosynthesis; IEA.
 DR GO; GO:0006597; P:spermine biosynthesis; IEA.
 DR InterPro; IPR001985; SAM decarbox.
 DR Pfam; PF01536; SAM decarbox; 1.
 DR ProDom; PD002379; SAM decarbox; 1.
 DR TIGRFAMs; TIGR00535; SAM_DCase; 1.
 DR PROSITE; PS01336; ADOMETDC; 1.
 SQ SEQUENCE 319 AA; 34854 MW; B0648B852F74A8E1 CRC64;

Query Match 61.5%; Score 1290; DB 2; Length 319;
 Best Local Similarity 89.6%; Pred. No. 3.2e-101;
 Matches 249; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 MAVLSAADASPVSAIGFEGYEKRLITFSEAPVFDPHGRLRALRAQIDSVLDLART 60
 DB 37 MGVLSSAADPPVSAIGFEGYEKRLITFSEAPVFDPHGRLRALRAQIDSVLDLART 96
 QY 61 IVSELNKPDSVYLSSESLFIYPLKIVKTCTGTTKLLLTIPRILELAELSMLAAYKY 120
 DB 97 IVSELNKPDSVYLSSESLFIYSDKIVKTCTGTTKLLLTIPRILELAELSMLAAYKY 156
 QY 121 SRGTFFPGAQAPHRFSFEVAVLNRYFGHLKSGGNAYVIGDPAPGQKWHVFYATEYP 180
 DB 157 SRGFTFFPGAQAPHRFSFEVAVLNRYFGHLKSGGNAYVIGDPAPGQKWHVYATQHP 216
 QY 181 EQPMVNLKMTGLDKKACVFFKTADGNNTTCAKEMTKLSGISEIIPMEICDPDFEPC 240
 DB 217 EQPMVNLKMTGLDKKACVFFKTADGNNTTCAKEMTKLSGISEIIPMEICDPDFEPC 276

QY 241 GYSMAIHGSAFTIHTVTPEDGFSYASYEVGMGLDATAL 278
 DB 277 GYSMAIHGSAFTIHTVTPEDGFSYASYEVGMGLDATAL 314

RESULT 12'
 QYXZQ9 PRELIMINARY; PRT; 358 AA.
 AC Q7XZQ9; 25, Created
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 26, Last annotation update)
 DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50).
 GN Names=saadc;
 OS Vitis vinifera (Grape).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Vitaceae; Vitis.
 OX NCBI_TaxID=29760;
 RN [1]
 RP TISSUE=Leaf.
 RA Tassoni A., Accetulli P., Bagni N.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ567368; CAD98785.1; -
 DR HSSP; P17707; IJEN.
 DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR GO; GO:0008295; P:spermidine biosynthesis; IEA.
 DR GO; GO:0006597; P:spermine biosynthesis; IEA.
 DR InterPro; IPR001985; SAM decarbox.
 DR Pfam; PF01536; SAM decarbox; 1.
 DR ProDom; PD002379; SAM decarbox; 1.
 DR TIGRFAMs; TIGR00535; SAM_DCase; 1.
 DR PROSITE; PS01336; ADOMETDC; 1.
 KW Lyase.
 FT CHAIN 2 358 S-adenosylmethionine decarboxylase.

SQ SEQUENCE 358 AA; 39783 MW; B6037EDA79132AE3 CRC64;

Query Match 47.7%; Score 1000; DB 2; Length 358;
 Best Local Similarity 53.4%; Pred. No. 1.8e-76;
 Matches 211; Conservative 51; Mismatches 85; Indels 48; Gaps 9;

QY 9 ASPVSAIGFEGYEKRLITFSEAPVFDPHGRLRALRAQIDSVLDLARTTIVSLSNK 68
 DB 2 ALPVSAGFEGYEKRLITFSEAPVFDPHGRLRALRAQIDSVLDLARTTIVSLSND 61
 QY 69 DFDSVYLSSESLFIYPLKIVKTCTGTTKLLLTIPRILELAELSMLAAYKISGTFFIP 128
 DB 62 IVDSVYLSSESLFIYVYPIKIITKCTGTTKLLLTIPRILELAELSMLAAYKISGTFFIP 121
 QY 129 GAQAPHRFSFEVAVLNRYFGHLKSGGNAYVIGDPAPGQKWHVFYATEYP--EQPMV 185
 DB 122 GAQAPHRFSFEVAVLNRYFGHLKSGGNAYVIGDPAPGQKWHVFYATEYP--EQPMV 180
 QY 186 NLEMCWTGLDKKACVFFKTADGNNTTCAKEMTKLSGISEIIPMEICDPDFEPCGYSMN 245
 DB 181 TLEMCWTGLDKKACVFFKTADGNNTTCAKEMTKLSGISEIIPMEICDPDFEPCGYSMN 236
 QY 246 AIHGSAFTIHTVTPEDGFSYASYEVGMGLDATALSYGDLVKRLVLCFSPSEFVSVAITFG 305
 DB 237 AIEGAASFTIHTVTPEDGFSYASYEVGMGLDATALSYGDLVKRLVLCFSPSEFVSVAITFG 291
 QY 306 RGHAGTWGK-----ALGAEVYDCNMVQELPGGGLLVYQSCAAEDAVATSPKSVFHC 359
 DB 292 --HADISGKLLERNCLLDVKGCCERSNEELCMGSMVYHRPMTKTEGLV--SPRSILKC 347
 QY 360 PDGENVESAPPMKKDYKLANLLCWEEEDADAMEEK 394
 DB 348 -----CWKEEEE--EEK 357

RESULT 13
 DCAM CATRO STANDARD; PRT; 357 AA.
 AC Q42679;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
 DE (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain].
 GN Name=SAMDC;
 OS Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Gentianales; Apocynaceae; Rauvolfioideae; Vinaceae;
 OC Catharanthus.
 OX NCBI_TaxID=4058;
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-71.
 RX MEDLINE=95188916; PubMed=7883014;
 RA Schroeder G., Schroeder J.;
 RT "cDNAs for S-adenosyl-L-methionine decarboxylase from Catharanthus roseus, heterologous expression, identification of the proenzyme-processing site, evidence for the presence of both subunits in the active enzyme, and a conserved region in the 5' mRNA leader.";
 RL Eur. J. Biochem. 228:74-78(1995).
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S)-deoxy-5-adenosyl(3-aminopropyl)-methylsulfonium salt + CO(2).
 CC -1- COFACTOR: Pyruvoyl group.
 CC -1- PATHWAY: decarboxylation of S-adenosylmethionine provides the aminopropyl moiety required for spermidine and spermine biosynthesis from putrescine.
 CC -1- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

NCBI TaxID=4096;
[1] SEQUENCE FROM N.A.
RA Nakakita M.;
RT "Putative cDNA for S-adenosylmethionine decarboxylase from Nicotiana sylvestris";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (5-deoxy-5-adenosyl) (3-aminopropyl)-methylsulfonium salt + CO(2).
CC -|- COFACTOR: Pyruvoyl group (By similarity).
CC -|- PATHWAY: Decarboxylation of S-adenosylmethionine provides the aminopropyl moiety required for spermidine and spermine biosynthesis from putrescine.
CC -|- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.
CC
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EMBL; AB015609; BAA29040.1; --
HSSP; P17707; 1JEN.
InterPro; IPR001985; SAM decarbox.
Pfam; PF01536; SAM decarbox; 1.
ProDom; PD002379; SAM decarbox; 1.
TIGRFAMs; TIGR00535; SAM DCase; 1.
PROSITE; PS01336; ADOMETDC; 1.
Decarboxylase; Lyase; Pyruvate; Spermidine biosynthesis; Zymogen.
CHAIN 1 72 S-adenosylmethionine decarboxylase beta chain (By similarity)
FT CHAIN 73 361 S-adenosylmethionine decarboxylase alpha chain (By similarity)
FT SITE 72 73 Pyruvic acid (Ser) (By similarity).
FT MOD_RES 73 73 Pyruvic acid (Ser) (By similarity).
FT ACT_SITE 13 13 By similarity.
FT ACT_SITE 16 16 By similarity.
FT ACT_SITE 87 87 By similarity.
FT ACT_SITE 361 361 By similarity.
SQ SEQUENCE 361 AA; 39681 MW; 648EB2F6CC61FFE CRC64;
Query Match 46.2%; Score 969; DB 1; Length 361;
Best Local Similarity 51.4%; Pred. No. 7.7e-74;
Matches 203; Conservative 49; Mismatches 97; Indels 46; Gaps 7;
QY 9 ASPVSAIGFEGYKRLLEITFSEAPVFDPHGRGLRALSRQAIDSVIDLARCTIVSELN 68
DB 2 ALPASAIGFEGYKRLLEISFFESFPADPDGKGLRALNKSQIDLEILPAECTIVDSLSNQ 61
QY 69 DFDYVLSSESLFIYPLKIVIKTCGTTKLLLTTPRILEAEELSMPLAAVKYRGTFIPP 128
DB 62 YLDSYVLSSESLFVYPIKTIKTCGTTKLLSIPAILKLAESLSVRNVKYYTRGSPFIP 121
QY 129 GAQPAPHRSEVAALNRYFGLKSGNAYVIGDPAPCGKWHVYFATPEQ---PMV 195
DB 122 GAQSPHRRSEVAALNRYFGLKSGNAYVIGDPAPCGKWHVYFATPEQ---PMV 195
QY 186 NLEMCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDPDFPCGYSMN 245
DB 181 TLEMCMTGLDREKASVYFKS---ESSAALMTTRSGIRKILPDSICDFEFPFCGYSMN 236
QY 246 AIHGSFSTHTVTPEDGFSYASVEVWGLDATALSYGDLVKRVLRCFCPSFESVAVTIFGG 305
DB 237 SIEEAAISTHTVTPEDGFSYASFEAAAGYDLKAQNLGMIVRLVACFPSEFSAV---- 291
QY 306 RGHAGTWGK-----ALGAEVYDCNNMVEQLPGGLLVYQSFCAAEADAVATSPKSVFHC 359
DB 292 --HCDVTCKSLQICSLDELKEYSLDEKINEELGLGGSIYKFLRID--ACGSPRSLKC 347
QY 360 FDGENVESAPPMKKDYKLANLLCWEEADAMEEK 394
DB 348 -----CWKE--DESEEE 357

RESULT 14
DCAM_NICSY STANDARD; PRT; 361 AA.
AC 080402;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
DE (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain].
GN Name=SAMDC1; Synonyms=SAMDC-1;
OS Nicotiana sylvestris (wood tobacco).
OC Eukaryota; Viridiplantae; Streptophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiids; Solanales; Solanaceae; Nicotiana.

OX NCBI_TaxID=4096;
RN [1] SEQUENCE FROM N.A.
RP Nakakita M.;
RA "Putative cDNA for S-adenosylmethionine decarboxylase from Nicotiana sylvestris";
RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RL -|- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (5-deoxy-5-adenosyl) (3-aminopropyl)-methylsulfonium salt + CO(2).
CC -|- COFACTOR: Pyruvoyl group (By similarity).
CC -|- PATHWAY: Decarboxylation of S-adenosylmethionine provides the aminopropyl moiety required for spermidine and spermine biosynthesis from putrescine.
CC -|- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; AB015609; BAA29040.1; --
HSSP; P17707; 1JEN.
InterPro; IPR001985; SAM decarbox.
Pfam; PF01536; SAM decarbox; 1.
ProDom; PD002379; SAM decarbox; 1.
TIGRFAMs; TIGR00535; SAM DCase; 1.
PROSITE; PS01336; ADOMETDC; 1.
Decarboxylase; Lyase; Pyruvate; Spermidine biosynthesis; Zymogen.
CHAIN 1 72 S-adenosylmethionine decarboxylase beta chain (By similarity)
FT CHAIN 73 361 S-adenosylmethionine decarboxylase alpha chain (By similarity)
FT SITE 72 73 Pyruvic acid (Ser) (By similarity).
FT MOD_RES 73 73 Pyruvic acid (Ser) (By similarity).
FT ACT_SITE 13 13 By similarity.
FT ACT_SITE 16 16 By similarity.
FT ACT_SITE 87 87 By similarity.
FT ACT_SITE 361 361 By similarity.
SQ SEQUENCE 361 AA; 39681 MW; 648EB2F6CC61FFE CRC64;
Query Match 46.2%; Score 969; DB 1; Length 361;
Best Local Similarity 51.4%; Pred. No. 7.7e-74;
Matches 203; Conservative 49; Mismatches 97; Indels 46; Gaps 7;
QY 9 ASPVSAIGFEGYKRLLEITFSEAPVFDPHGRGLRALSRQAIDSVIDLARCTIVSELN 68
DB 4 ALPASAIGFEGYKRLLEISFFESFPADPDGKGLRALNKSQIDLEILPAECTIVDSLSND 63
QY 69 DFDYVLSSESLFIYPLKIVIKTCGTTKLLLTTPRILEAEELSMPLAAVKYRGTFIPP 128
DB 64 DFDYVLSSESLFVYPIKTIKTCGTTKLLSIPAILKLAETLSLKVQDVYTRGSPFIP 123
QY 129 GAQPAPHRSEVAALNRYFGLKSGNAYVIGDPAPCGKWHVYFATPEQ---PMV 185
DB 124 GAQSPHRRSEVAALNRYFGLKSGNAYVIGDPAPCGKWHVYFATPEQ---PMV 185
QY 186 NLEMCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDPDFPCGYSMN 245
DB 183 TLEMCMTGLDREKASVYFKTEG---SSAAMTVRSGIRKILPNSBEICDFEFPFCGYSMN 238
QY 246 AIHGSFSTHTVTPEDGFSYASVEVWGLDATALSYGDLVKRVLRCFCPSFESVAVTIFGG 305
DB 239 SIEEAAISTHTVTPEDGFSYASFEAAAGYDMKTKMLGVLVRLVACFPSEFSAV---- 293
QY 306 RGHAGTWGK-----ALGAEVYDCNNMVEQLPGGLLVYQSFCAAEADAVATSPKSVFHC 359
DB 294 --HADVATKLLERVCSDVKGYSLAEWSPEEFCKGGSIVYQK--TTPPCGSPKSVLKG 349
QY 360 FDGENVESAPPMKKDYKLANLLCWEEADAMEEK 394
DB 350 -----CWKEDEEKEE 361

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Db      4  ALPVSAGPFGPEKRLSEISFEFGLFADPNCKGLRSLSKAQLDEILGPACTIVDSLND 53
Qy      69  DFDOSYVLSSESLFTYPLKVIKTCGTTKKLLLTIPRIIELEABELSNPLAAVYSRGTFFP 128
Db      64  DVDSYVLSSESLFVYSYKIIITKCGTTKLIAIPIILKLAETLSLKQDVRYTRGSGFFP 123
Qy      129  GAQPAPHRFSFSEEAALNRRYFEGGLKSGGNVVICDPARPQOKWHVFYATEPEQ---PMV 185
Db      124  GAQSFPHRHSFSEEAVALJDFGFKLAGSKAVIMGSPDK-AQKWHVYSASAGPIQNDPVY 182
Qy      186  NLEMCMTGLDKKACVPFFKTNADGNTT'CAKEMTKLSGTSEIIPMEIICDFPEPCGYSMN 245
Db      183  TLEMCMTGLDREKASVFKYKTEG---SSAAHMTVRSRGIRKILPNSEICDFEFPCGYSMN 238
Qy      246  AIHGSAPSTHTVTPEDGFSVASYEVMGLDATALSYGDLVKRVLRCFGSSEFSVATIFGG 305
Db      239  SIEGAALSTHTIIPEDGFSVASFVAGYDMKTKLGPLVERVLACFEPEDFSIAL----- 293
Qy      306  RHAGTGWKAL-----GAEYDCNNVVEOELPCGGLLLVYQSFCAEAEDAVATSPKSVFHC 359
Db      294  --HADVATKULERVCSYVDVVGYSLAEWSPEEFGKGGSIVYOKF--TRTPFCGSPKSVLKG 349
Qy      360  FDGENVESAPPMKKOYKLANLLCWEESADEAMEEK 394
Db      350  -----CWKEDEEKEKE 361

Search completed: May 11, 2005, 22:52:30
Job time : 95.5017 secs

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